

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 23, 2005, 08:26:40 ; Search time 72.4256 Seconds

(without alignments)
4426.083 Million cell updates/sec

Title: US-10-073-064-5
Perfect score: 3338
Sequence: 1 MVVQTRPPSWIILCYMLG.....DGMETQHNKKMIASCSRL 626

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:
1: uniprot_sprot:
2: uniprot_trembl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|-------------|
| 1 | 3195 | 95.7 | 610 | 2 | O8CC52 |
| 2 | 3191 | 95.6 | 998 | 1 | EPB7_MOUSE |
| 3 | 3187.5 | 95.5 | 994 | 2 | O8R3B1 |
| 4 | 3187 | 95.5 | 998 | 2 | O8BSU8 |
| 5 | 3175 | 95.1 | 998 | 1 | EPB7_RAT |
| 6 | 3139 | 94.0 | 998 | 1 | EPB7_HUMAN |
| 7 | 3126 | 93.6 | 593 | 2 | O8C7N2 |
| 8 | 3031.5 | 90.8 | 993 | 1 | EPB7_CHICK |
| 9 | 1860.5 | 55.7 | 681 | 2 | O8C276 |
| 10 | 1819 | 54.5 | 1005 | 1 | EPB5_RAT |
| 11 | 1817 | 54.4 | 1037 | 1 | EPB5_HUMAN |
| 12 | 1800 | 53.9 | 1013 | 1 | EPB5_CHICK |
| 13 | 1799 | 53.9 | 984 | 2 | O8BRB1 |
| 14 | 1796 | 53.8 | 983 | 1 | EPB3_HUMAN |
| 15 | 1796 | 53.8 | 983 | 2 | O6P4R6 |
| 16 | 1795.5 | 53.8 | 986 | 1 | EPB4_XENLA |
| 17 | 1795 | 53.8 | 984 | 2 | O8C3U1 |
| 18 | 1790.5 | 53.6 | 985 | 1 | EPB4_XENLA |
| 19 | 1789.5 | 53.6 | 986 | 2 | O7ZYM7 |
| 20 | 1788 | 53.6 | 969 | 2 | O7Z3F2 |
| 21 | 1787.5 | 53.6 | 984 | 1 | EPB3_RAT |
| 22 | 1783.5 | 53.4 | 983 | 1 | EPB3_CHICK |
| 23 | 1783.5 | 53.4 | 983 | 1 | EPB3_MOUSE |
| 24 | 1782.5 | 52.5 | 986 | 1 | EPB4_CHICK |
| 25 | 1741.5 | 52.2 | 986 | 1 | EPB4_HUMAN |
| 26 | 1739 | 52.1 | 538 | 2 | O8C9K6 |
| 27 | 1728 | 51.8 | 986 | 2 | O8QVZ2 |
| 28 | 1723 | 51.6 | 986 | 1 | EPB4_MOUSE |
| 29 | 1701.5 | 51.0 | 1005 | 1 | EPB8_HUMAN |
| 30 | 1695 | 50.8 | 1004 | 1 | EPB8_MOUSE |
| 31 | 1655 | 49.6 | 948 | 1 | EPB6_RAT |
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ALIGNMENTS

| RESULT 1 | | | | | | | | | |
|----------|---|-------------|--------|----|-------------|-------------|---------|--------|--------|
| ID | Score | Query Match | Length | ID | Description | Accession | Species | Strain | Source |
| O8CC52 | 3195 | 95.7 | 610 | 2 | O8CC52 | PRELIMINARY | PRT | 610 AA | |
| AC | O8CC52 | | | | | | | | |
| DT | 01-MAR-2003 | | | | | | | | |
| DT | 01-MAR-2003 | | | | | | | | |
| DT | 01-MAR-2004 | | | | | | | | |
| DE | Mus musculus adult male diencephalon cDNA, Riken full-length enriched library, clone:9330112M1 product:Epn receptor A7, full insert sequence. | | | | | | | | |
| GN | Name=Bpha7 | | | | | | | | |
| OS | Mus musculus (Mouse) | | | | | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | | | | | | |
| OX | NCBI_Taxid=10090 | | | | | | | | |
| RN | [1] | | | | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | | | | |
| RC | STRAIN=C57BL/6J; TISSUE=Diencephalon; | | | | | | | | |
| RX | MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; | | | | | | | | |
| RA | Carpinci P., Hayashizaki Y.; | | | | | | | | |
| RT | "High-efficiency full-length cDNA cloning."; | | | | | | | | |
| RL | Mech. Enzymol. 303:19-44(1999). | | | | | | | | |
| RN | [2] | | | | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | | | | |
| RC | STRAIN=C57BL/6J; TISSUE=Diencephalon; | | | | | | | | |
| RX | MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500; | | | | | | | | |
| RA | RIKEN FANTOM Consortium; | | | | | | | | |
| RT | "Functional annotation of a full-length mouse cDNA collection."; | | | | | | | | |
| RL | Nature 409:685-690(2001). | | | | | | | | |
| RN | [3] | | | | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | | | | |
| RC | STRAIN=C57BL/6J; TISSUE=Diencephalon; | | | | | | | | |
| RA | The FANTOM Consortium; | | | | | | | | |
| RT | "Analysis of the mouse transcripome based on functional annotation of 60,770 full-length cDNAs."; | | | | | | | | |
| RL | Nature 420:563-573(2002). | | | | | | | | |
| RN | [4] | | | | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | | | | |
| RC | STRAIN=C57BL/6J; TISSUE=Diencephalon; | | | | | | | | |
| RX | MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; | | | | | | | | |
| RA | Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.; | | | | | | | | |
| RT | "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; | | | | | | | | |
| RL | Genome Res. 10:1617-1630(2000). | | | | | | | | |
| RN | [5] | | | | | | | | |
| RP | SEQUENCE FROM N.A. | | | | | | | | |
| RC | STRAIN=C57BL/6J; TISSUE=Diencephalon; | | | | | | | | |
| RX | MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; | | | | | | | | |
| RA | Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Kono H., Akiyama U., Nishi K., Kitounai T., Tashiro H., Itoh M., Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., | | | | | | | | |

RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai Y.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "MIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN 161
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
 RA Aachai J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
 RA Hori F., Imotani K., Ishi Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Komoto H., Kouda M., Koya S.,
 RA Kuchihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,
 RA Saito R., Sakita H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tomaru A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK033903; BAC28509.1; -
 DR HSSP; P54763; INUK.
 DR MGD; MGI:95276; Epha7.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR001090; Ephrin_receptor.
 DR InterPro; IPR003962; Fcrl1 subd.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR008979; Gal_bind-like.
 DR InterPro; IPR009030; Grow_fac_recept.
 DR InterPro; IPR001426; Ykase_receptorV.
 DR Pfam; PF01404; Ephrin_1bd; 1.
 DR Pfam; PF00041; Fn3; 1.
 DR PRINTS; PR00014; FNTYPEIII.
 DR PRODOM; PD001495; Ephrin_receptor; 1.
 DR SMART; SM00615; EPH_1bd; 1.
 DR SMART; SM00060; FN3; 2.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS50853; FN3; 2.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 KW Receptor.
 SQ SEQUENCE 610 AA; 68285 MW; E61310A72FBE1E739 CRC64;
 Query Match 95.7%; Score 3195; DB 2; Length 61c;
 Best Local Similarity 99.8%; Pred. No. 1.3e-230; Indels 0; Gaps 0;
 Matches 600; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MVTQTRPPSWIIICYLWLGFAHTGSAQAKEVLLLDLSKAQOLETEWISPPSGWEISIG 60
 DB 1 MVTQTRPPSWIIICYLWLGFAHTGSAQAKEVLLLDLSKAQOLETEWISPPSGWEISIG 60
 QY 61 LDENVPIRIRYQVCQWEPNOMNLRNWSKGAQRIPELKFITLDDCKSLPQVATGCK 120
 DB 61 LDENVPIRIRYQVCQWEPNOMNLRNWSKGAQRIPELKFITLDDCKSLPQVATGCK 120
 QY 121 EFTNLYYYETDYPDGRIRIRNLYVKIDITIADESFTQGDGGERMKKNTVREIGPLSKK 180
 DB 121 EFTNLYYYETDYPDGRIRIRNLYVKIDITIADESFTQGDGGERMKKNTVREIGPLSKK 180
 QY 181 GFYLAPODVACIALVSVKYYKKCWITVENLAVFPDVTGSEFSSSLVEVGTCSAAE 240
 DB 181 GFYLAPODVACIALVSVKYYKKCWITVENLAVFPDVTGSEFSSSLVEVGTCSAAE 240
 QY 241 EAENSPPMHSABGEWLVPIGCKTCKAGYQOQKGTCPGCGRRYKSSQQLQCSRCPTHS 300
 DB 241 EAENSPPMHSABGEWLVPIGCKTCKAGYQOQKGTCPGCGRRYKSSQQLQCSRCPTHS 300
 QY 301 FSDREGSRCECEGGYRAPSDPYVACTPPSAPQULININQTTVLSLWSPADNGR 360
 DB 301 FSDREGSRCECEGGYRAPSDPYVACTPPSAPQULININQTTVLSLWSPADNGR 360

DB 301 FSDREGSRCECEGGYRAPSDPYVACTPPSAPQULININQTTVLSLWSPADNGR 360
 QY 361 NDVTYRILCKRCSEWEGECVPCSGNIGYMPQOTGEDNVTYVMDLAAHYTFEEVAVG 420
 DB 361 NDVTYRILCKRCSEWEGECVPCSGNIGYMPQOTGEDNVTYVMDLAAHYTFEEVAVG 420
 QY 421 VSDLSRSQRLFAVSTTTGQAAPSQVSGYMKERVLORSVLSQGEPEHNGVTTEIKY 480
 DB 421 VSDLSRSQRLFAVSTTTGQAAPSQVSGYMKERVLORSVLSQGEPEHNGVTTEIKY 480
 QY 481 YEEDQERRTYSLTKTSTASINNLKPGTYVYFOIRAVTAAGYNSPRLDVATLEASG 540
 DB 481 YEEDQERRTYSLTKTSTASINNLKPGTYVYFOIRAVTAAGYNSPRLDVATLEASG 540
 QY 541 KMEATVASEQNPVITIAVAVAGTIIIVFWFGFIIGRRHCGYSKADQEGDELYFHS 600
 DB 541 KMEATVASEQNPVITIAVAVAGTIIIVFWFGFIIGRRHCGYSKADQEGDELYFHS 600
 QY 601 L 601
 DB 601 L 601
 RESULT 2
 EBP7_MOUSE STANDARD; PRT; 998 AA.
 ID EBP7_MOUSE
 AC Q61772; Q61505; Q61773; Q61774;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ephrin type-A receptor 7 precursor (EC 2.7.1.112) (Tyrosine-protein
 DE kinase receptor EHK-3) (EPH homolog kinase-3) (Embryonic brain
 DE kinase) (EBK) (Developmental kinase 1) (MDK-1).
 GN Name=Epha7; Synonyms=EbK; Ehk3; Mdk1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC STRAIN=BALB/c; TISSUE=Brain;
 RX MEDLINE=95124729; PubMed=7824284;
 RA "Closek T., Milbauer B., Ullrich A.;
 RA "Identification of alternatively spliced mRNAs encoding variants of
 RT MDK1, a novel receptor tyrosine kinase expressed in the murine nervous
 RT system.";
 RL Oncogene 10:97-106(1995).
 RN (2)
 RP SEQUENCE OF 431-998 FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=96081374; PubMed=8541219; DOI=10.1016/0925-4773(95)00411-S;
 RA Ellis J., Liu Q., Bretzman M., Jenkins N.A., Gilbert D.J.,
 RA Copeland N.G., Tempest H.V., Warren S., Muir E., Schilling H.,
 RA Fletcher F.A., Ziegler S.F., Rogers J.H.;
 RT "Embryo brain kinase: a novel gene of the eph/elk receptor tyrosine
 RT kinase family.";
 RL Mech. Dev. 52:319-341(1995).
 RN (3)
 RP INTERACTIONS WITH PRKCA AND GRIP1.
 RX MEDLINE=9098206; PubMed=9883737; DOI=10.1016/S0896-6273(00)80663-7;
 RA Torres R., Firestein B.L., Dong H., Staudinger J., Olson E.N.,
 RA Huganir R.L., Bredt D.S., Gale N.W., Yancopoulos G.D.;
 RT "PDZ proteins bind, cluster, and synaptically colocalize with Eph
 RT receptors and their ephrin ligands.";
 RL Neuron 21:1453-1463(1998).
 CC -1- FUNCTION: Receptor for members of the ephrin-A family. Binds to
 CC ephrin-A1, -A2, -A3, -A4 and -A5.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBUNIT: Interacts with PRKCA and GRIP1.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=5;

```

CC      Name=1; Synonyms=MDK1;
CC      IsoId=Q61772-1; Sequence=Displayed;
CC      Name=2; Synonyms=MDK1-1;
CC      IsoId=Q61772-2; Sequence=VSP_003006;
CC      Name=3; Synonyms=MDK1-2;
CC      IsoId=Q61772-3; Sequence=VSP_003007;
CC      Name=4; Synonyms=MDK1-T1;
CC      IsoId=Q61772-4; Sequence=VSP_003008; VSP_003009;
CC      Name=5; Synonyms=MDK1-T2;
CC      IsoId=Q61772-5; Sequence=VSP_003010; VSP_003011;
CC      - TISSUE SPECIFICITY: Widely expressed in embryo. In adult,
CC      expression restricted to hippocampus, testis and spleen.
CC      - SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin
CC      receptor subfamily.
CC      - SIMILARITY: Contains 2 fibronectin type III domains.
CC      - SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC      the European Bioinformatics Institute. There are no restrictions on
CC      use by non-profit institutions as long as their content is in no way
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CC      entities requires a license agreement (see http://www.isb-sib.ch/announce
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; X79082; CAA55687.1; -;
DR      EMBL; X79083; CAA55688.1; -;
DR      EMBL; X79084; CAA55689.1; -;
DR      EMBL; X81466; CAA57224.1; -;
DR      PIR; I48612; I48612.
DR      PIR; I48614; I48614.
DR      PIR; JCS672; JCS672.
DR      HSSP; P54763; IJPA.
DR      MGD; MGI:95276; EphA7.
DR      InterPro; IPR006209; EGF_like.
DR      InterPro; IPR001090; Ephrin_receptor.
DR      InterPro; IPR003961; FN_III.
DR      InterPro; IPR008957; FN_III-like.
DR      InterPro; IPR003962; FNIII_subd.
DR      InterPro; IPR008979; Gal_bind_like.
DR      InterPro; IPR009030; Grow_fac_recept.
DR      InterPro; IPR011009; Kinase_like.
DR      InterPro; IPR000719; Prot_kinase.
DR      InterPro; IPR001660; SAM.
DR      InterPro; IPR001245; Tyr_kinase.
DR      InterPro; IPR008266; Tyr_kinase_AS.
DR      InterPro; IPR001426; Ykase_receptorV.
DR      Pfam; PF01404; Ephrin_1bd; 1.
DR      Pfam; PF00041; fn3_2.
DR      Pfam; PF00069; Kinase; 1.
DR      Pfam; PF00536; SAM; 1.
DR      PRINTS; PR00014; FNTYPEIT1.
DR      PRINTS; PR00109; TYRKINASE.
DR      ProDom; PD001495; Ephrin_receptor; 1.
DR      ProDom; PD000001; Prot_kinase; 1.
DR      SMART; SM00615; EPH_1bd; 1.
DR      SMART; SM00060; FN3_2.
DR      SMART; SM00454; SAM; 1.
DR      SMART; SM00219; TYRkc; 1.
DR      PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR      PROSITE; PS50853; FN3_2.
DR      PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR      PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR      PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR      PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR      PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR      PROSITE; PS50105; SAM_DOMAIN; 1.
KW      Alternative splicing; ATP-binding; Glycoprotein; Phosphorylation;
KW      Receptor; Repeat; Signal; Transferrase; Transmembrane;
KW      Tyrosine-protein kinase.
KT      SIGNAL 1 29 Potential.
KT      CHAIN 30 998 Ephrin type-A receptor 7.
KT      DOMAIN 30 556 Extracellular (Potential).

```

[illegible]

Db 421 VSDLSRQRLFAVSTITGOAPSPQVSGMKERYLQSRVOLSKOEPHEHNGVITEYEIKY 480
 QY 481 YEKDQREERTYSTLTKSTASINNLKPGTYVFOIRAVTAAGYNSPRLDVAATLEBASG 540
 Db 481 YEKDQREERTYSTLTKSTASINNLKPGTYVFOIRAVTAAGYNSPRLDVAATLEBASG 540
 QY 541 KMEFATVSSSEQNPVITIAVAVAGTIIIVFMVFGFIIGRHCGYSKADQDEJDELYFH 599
 Db 541 KMEFATVSSSEQNPVITIAVAVAGTIIIVFMVFGFIIGRHCGYSKADQDEJDELYFH 599
 RESULT 3
 QSR381 PRELIMINARY; PRT; 994 AA.
 ID QSR381
 AC QSR381;
 DT 01-JUN-2002 (TREMblrel. 21, Created)
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
 DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
 DE Bphat7 protein.
 GN Name=Bphat7;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C2CEH II; TISSUE=Mammary tumor;
 RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derje J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Tosihyuki S., Carninci P., Prange C.J.,
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muljany S.J.,
 RA Bosak S.A., McKernan P.U., McKernan K.J., Malek J.A., Gnarutene P.H.,
 RA Richards S., Wooley K.C., Hale S., Garcia A.M., Gay L.V., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzyzanski M.I., Skalska U., Smallie D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C2CEH II; TISSUE=Mammary tumor;
 RA Strausberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 CC -|- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -|- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
 CC -|- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin
 CC receptor subfamily.
 DR EMBL: BC026153; AAH26153.1; -.
 DR HSSP: P54763; ItpA.
 DR MGD: MGI:95276; Epha7.
 DR GO: GO:0005615; C:intracellular space; TAS.
 DR GO: GO:0016021; C:integral to membrane; TAS.
 DR InterPro: IPR006209; EGF like.
 DR InterPro: IPR001090; Ephrin receptor.
 DR InterPro: IPR003962; PhII subd.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR008957; FN_III-like.
 DR InterPro: IPR008979; Gal_bind like.
 DR InterPro: IPR009030; Grow_fac recept.
 DR InterPro: IPR011009; Kinase like.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR001660; SAM.

DR InterPro: IPR001245; Tyr_kinase.
 DR InterPro: IPR008266; Tyr_kinase_AS.
 DR InterPro: IPR001426; Ykase_receptorV.
 DR Pfam: PF01404; Ephrin_1bd; 1.
 DR Pfam: PF00041; fn3_1.
 DR Pfam: PF00536; SAM_1.1.
 DR PRINTS: PR00014; FNTPETII.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD001495; Ephrin_receptor; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00615; EPH_1bd; 1.
 DR SMART: SM00060; FN3_2.
 DR SMART: SM00454; SAM; 1.
 DR SMART: SM00219; Tyrc; 1.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS50853; FN3_2.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS50011; PROTEIN KINASE_DOM; 1.
 DR PROSITE: PS00109; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE: PS50105; SAM_DOMAIN; 1.
 DR ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;
 KM Transferase; Transmembrane; Tyrosine-protein kinase
 SQ SEQUENCE 994 AA; 11138 MW; A28F98BD94F2EB8 CRC64;
 Query Match 95.5%; Score 3187.5; DB 2; Length 994;
 Best Local Similarity 95.7%; Pred. No. 9.6e-230;
 Matches 604; Conservative 7; Mismatches 15; Indels 5; Gaps 2;
 QY 1 MVTQTPSPWIIICITWILGFAHTGEAOAKVELLDLSAQOQTELEWISSPPSGMEISG 60
 Db 1 MVTQTPSPWIIICITWILGFAHTGEAOAKVELLDLSAQOQTELEWISSPPSGMEISG 60
 QY 61 LDENYPIPTIYQYQVMEPNQNNMLRTNWSKGNARIVELKFTLRDCNSLPGVGTCK 120
 Db 61 LDENYPIPTIYQYQVMEPNQNNMLRTNWSKGNARIVELKFTLRDCNSLPGVGTCK 120
 QY 121 EFTNLYYETDVTGGRNIRENLVYKIDTIADESFTQDGLGERKMLNTEVREIGPLSKK 180
 Db 121 EFTNLYYETDVTGGRNIRENLVYKIDTIADESFTQDGLGERKMLNTEVREIGPLSKK 180
 QY 181 GFPLAODVGCALYVSVYVYKCKWTIYENLAVFPDVTYTSRFSLLVEVRGCVSSABE 240
 Db 181 GFPLAODVGCALYVSVYVYKCKWTIYENLAVFPDVTYTSRFSLLVEVRGCVSSABE 240
 QY 241 EAENSFRMCSABGEVLVPIGKICCAAGYQOKGDTCEPCGRFPYKSSSODLQCSRCPYHS 300
 Db 241 EAENSFRMCSABGEVLVPIGKICCAAGYQOKGDTCEPCGRFPYKSSSODLQCSRCPYHS 300
 QY 301 FSDREGSSRCCEDEGYRAAPSDPYVACTRPPAPQNLIFINQTVSLJEMSPADNGCR 360
 Db 301 FSDREGSSRCCEDEGYRAAPSDPYVACTRPPAPQNLIFINQTVSLJEMSPADNGCR 360
 QY 361 NDVTYIILCKRGWEGECYPCGSNIGYMPQDTGLENDYVYVMDLAAHNYTFEVAUNG 420
 Db 361 NDVTYIILCKRGWEGECYPCGSNIGYMPQDTGLENDYVYVMDLAAHNYTFEVAUNG 420
 QY 421 VSDLSRQRLFAVSTITGOAPSPQVSGMKERYLQSRVOLSKOEPHEHNGVITEYEIKY 480
 Db 421 VSDLSRQRLFAVSTITGOAPSPQVSGMKERYLQSRVOLSKOEPHEHNGVITEYEIKY 480
 QY 481 YEKDQREERTYSTLTKSTASINNLKPGTYVFOIRAVTAAGYNSPRLDVAATLEBASG 540
 Db 481 YEKDQREERTYSTLTKSTASINNLKPGTYVFOIRAVTAAGYNSPRLDVAATLEBASG 540
 QY 541 KMEFATVSSSEQNPVITIAVAVAGTIIIVFMVFGFIIGRHCGYSKADQDEJDELYFH 600
 Db 541 KMEFATVSSSEQNPVITIAVAVAGTIIIVFMVFGFIIGRHCGYSKADQDEJDELYFH 600
 QY 601 ---LYRERGDMKTKQHN-KKKMILASGRL 626
 Db 601 TKTYIDPETYEEDPNRAVHOPAKELDASCITKI 631

RESULT 4
Q8BS08 PRELIMINARY; PRT; 998 AA.
ID Q8BS08
AC Q8BS08
DT 01-MAR-2003 (TRENBLurel. 23, Created)
DT 01-MAR-2003 (TRENBLurel. 23, Last sequence update)
DT 01-MAR-2004 (TRENBLurel. 26, Last annotation update)
DE Mus musculus adult male pituitary gland cDNA, RIKEN full-length
DE enriched library, clone:530417H08 product:EpH receptor A7, full
DE insert sequence.
GN Name=EphA7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=pituitary gland;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.,
RT "High-efficiency full-length cDNA cloning.",
RL Mech. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=pituitary gland;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.",
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=pituitary gland;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.",
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=pituitary gland;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.",
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=pituitary gland;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Azawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Itoh M.,
RA Suni N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.",
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=pituitary gland;
RA Adachi J., Azawa K., Akimura T., Hara A., Hashizume W.,
RA Fukuda S., Furuno M., Hasegaki T., Hiraoka T., Hirozane T.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hironaka T.,
RA Hori F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kanukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin
CC receptor subfamily.
DR EMBL; AK030460; BAC26982.1; -.
DR HSSP; P54763; 1JPA.
DR MGD; MGI:95276; EphA7.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR006209; BGF_1like.
DR InterPro; IPR001090; Ephrin_receptor.
DR InterPro; IPR003962; FNIII_subd.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-1like.
DR InterPro; IPR008979; Gal_bind_1like.
DR InterPro; IPR009030; GROW_fac_recept.
DR InterPro; IPR011009; Kinase_1like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001660; SAM.
DR InterPro; IPR01245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR InterPro; IPR001426; YKase_receptorV.
DR Pfam; PF01404; Ephrin_1bd; 1.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00536; SAM_1; 1.
DR PRINTS; PR00104; FNTYPEIII.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD001495; Ephrin_receptor; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00615; Eph_1bd; 1.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00454; SAM; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00853; FN3; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PS01005; SAM_DOMAIN; 1.
KW ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;
KW Transferrase; Transmembrane; Tyrosine-protein kinase.
SQ SEQUENCE 998 AA; 11859 MW; FCA1B83490E746E1 CRC64;
Query Match 95.5%; Score 3187; DB 2; Length 998;
Best Local Similarity 99.8%; Pred. No. 1.1e-229;
Matches 598; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MVVOTRPPSWIILCYIWLGFATGEGQAKEVLLDLSKQOQTELEWISSPPSGMERISG 60
Db 1 MVVOTRPPSWIILCYIWLGFATGEGQAKEVLLDLSKQOQTELEWISSPPSGMERISG 60
Qy 61 LDENVYTRIRYOVQVMEPNQNNWLRITNWSKGNQRIPELKTLLDQNSLPGLGTCK 120
Db 61 LDENVYTRIRYOVQVMEPNQNNWLRITNWSKGNQRIPELKTLLDQNSLPGLGTCK 120
Qy 121 ETPNLYYFNDYDTGRIRENLYKIDITIADESFTGGDGERMKNTVREIGPSKK 180
Db 121 ETPNLYYFNDYDTGRIRENLYKIDITIADESFTGGDGERMKNTVREIGPSKK 180
Qy 181 GFYLAPODVACIALVSKYIKKQWTIVENLAVFPDTVGSSESSLVEVRCVSSAE 240
Db 181 GFYLAPODVACIALVSKYIKKQWTIVENLAVFPDTVGSSESSLVEVRCVSSAE 240
Qy 241 EAENSPRMHCSAEGEWLVPIGKCI CKAGYQOKGDTCPGRRFRYKSSSDQLQCSRCPTH 300
Db 241 EAENSPRMHCSAEGEWLVPIGKCI CKAGYQOKGDTCPGRRFRYKSSSDQLQCSRCPTH 300

QY 301 FSDREGSSRCCEGDGYRAPSDPPYVACTRPPSAPQMLFININQTVLSLMSPPADNGCR 360
 DB 301 FSDREGSSRCCEGDGYRAPSDPPYVACTRPPSAPQMLFININQTVLSLMSPPADNGCR 360
 QY 361 NDVTYRILCRKCSWGECECPGCSNIGYMPQGTGLENNYTTVDLMAHYTTEVAVNG 420
 DB 361 NDVTYRILCRKCSWGECECPGCSNIGYMPQGTGLENNYTTVDLMAHYTTEVAVNG 420
 QY 421 VSDLSRSQRLFAAVSITTGGAAPQVSGWKEKERYLQSVLSMOEPHNGVITTEYIKY 480
 DB 421 VSDLSRSQRLFAAVSITTGGAAPQVSGWKEKERYLQSVLSMOEPHNGVITTEYIKY 480
 QY 481 YEKDQERRTYSLTKTKSTASINNLKRGTYVFPQIRAVTAAGYGNVSPRLVATLEBASG 540
 DB 481 YEKDQERRTYSLTKTKSTASINNLKRGTYVFPQIRAVTAAGYGNVSPRLVATLEBASG 540
 QY 541 KMEATVASSSEQNPVILIAVAVAGTILVFMVGFILGRHCGYSKADQIGDELYEH 599
 DB 541 KMEATVASSSEQNPVILIAVAVAGTILVFMVGFILGRHCGYSKADQIGDELYEH 599

RESULT 5
 EPR7 RAT STANDARD; PRT; 998 AA.
 ID EPR7 RAT STANDARD; PRT; 998 AA.
 AC P54759;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Ephrin type-A receptor 7 precursor (EC 2.7.1.112) (Tyrosine-protein
 kinase receptor Etk-3) (EPH homology kinase-3).
 GN Name=Epha7; Synonyms=Etk-3, Etk3;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
 RX MEDLINE=95249272; PubMed=7731712;
 RA Valenzuela D.M., Rojas E., Griffiths J.A., Compton D.L., Gisser M.,
 RA Ip N.Y., Goldfarb M., Yancopoulos G.D.;
 RT "Identification of full-length and truncated forms of Etk-3, a novel
 RT member of the Eph receptor tyrosine kinase family.";
 RL Oncogene 10:1573-1580(1995).
 CC -1- FUNCTION: Receptor for members of the ephrin-A family. Binds to
 CC ephrin-A1, -A2, -A3, -A4 and -A5.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC -1- tyrosine phosphate. Interacts with PRKCAP and GRIP1 (By similarity).
 CC -1- SUBUNIT: Interacts with PRKCAP and GRIP1 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=long;
 CC IsoId=B54759-1; Sequence=Displayed;
 CC Note=More widely expressed in the embryo;
 CC Name=short;
 CC IsoId=B54759-2; Sequence=VSP_003012;
 CC Note=Lacks the kinase domain;
 CC -1- TISSUE SPECIFICITY: Restricted to the nervous system.
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin
 CC receptor subfamily.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
 CC or send an email to license@ebi.ac.uk).
 CC EMBL; U21954; AAA86830.1; -.

DR EMBL; U21955; AAA86831.1; -.
 DR HSSP; P54763; 1UPA.
 DR RGD; 70957; Epha7.
 DR InterPro; IPR006209; BGF-like.
 DR InterPro; IPR001090; Ephrin_receptor.
 DR InterPro; IPR003964; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR008979; Gal_bind-like.
 DR InterPro; IPR009030; Grow_fac_recept.
 DR InterPro; IPR011009; Kinase-like.
 DR InterPro; IPR007719; Prot_kinase.
 DR InterPro; IPR001660; SAM.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR InterPro; IPR001426; YKase_receptorV.
 DR Pfam; PR01404; Ephrin_Ibd; 1.
 DR Pfam; PF00041; fn3_2.
 DR Pfam; PF00069; Kinase; 1.
 DR Pfam; PF00536; SAM; 1.
 DR PRINTS; PR00014; ENTPEIIT.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD001495; Ephrin_receptor; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00615; EPH_Ibd; 1.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00454; SAM; 1.
 DR SMART; SM00219; TYKc; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS08853; FN3_2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS50105; SAM_DOMAIN; 1.
 DR KW Alternative splicing; ATP-binding; Glycoprotein; Phosphorylation;
 DR KW Receptor; Repeat; Signal; Transferrase; Transmembrane;
 DR KM Tyrosine-protein kinase.
 FT SIGNAL 1 24
 FT CHAIN 25 998
 FT DOMAIN 25 556
 FT TRANSMEM 557 577
 FT DOMAIN 578 998
 FT DOMAIN 192 328
 FT DOMAIN 331 433
 FT DOMAIN 443 535
 FT DOMAIN 633 894
 FT DOMAIN 923 987
 FT SITE 996 998
 FT NP_BIND 639 647
 FT BINDING 665 665
 FT ACT_SITE 758 758
 FT MOD_RES 608 608
 FT MOD_RES 614 614
 FT MOD_RES 791 791
 FT MOD_RES 940 940
 FT CARBOHYD 343 343
 FT CARBOHYD 410 410
 FT VARSPIC 600 610

Query Match 95.1%; Score 3175; DB 1; Length 998;
 Best Local Similarity 99.2%; Pred. No. 8.3e-229;
 Matches 594; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVTQTRPPSWIILCYWILGFPHATGEAQAKEYLLDLSKAQOTLEWISSPPSGMEEISG 60

| | | | | |
|--|--|---|-----------------------------------|---|
| FT | MOD_RES | 614 | 614 | Phosphotyrosine (by autocatalysis) (potential). |
| FT | MOD_RES | 791 | 791 | Phosphotyrosine (by autocalysis) (potential). |
| FT | MOD_RES | 940 | 940 | Phosphotyrosine (by autocalysis) (potential). |
| FT | CARBOHYD | 343 | 343 | N-linked (GlcNAc. . .) (potential). |
| FT | CARBOHYD | 410 | 410 | N-linked (GlcNAc. . .) (potential). |
| SO | SEQUENCE | 998 AA; | 112096 MW; 4798CA0D2BB06EB CRC64; | |
| Query Match | | | | |
| Best Local Similarity 97.7%; Score 3139; DB 1; Length 998; | | | | |
| Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0 | | | | |
| OY | 1 | MVQTRFSPWIIICYLWLGFAHTGEAOAAKEVLLDLSKAQOQTELEWISSEPSGWEIISG | 60 | |
| Db | 1 | MVFQTRYSWIIICYLWILRFHAHTGEAOAAKEVLLDLSKAQOQTELEWISSEPSGWEIISG | 60 | |
| OY | 61 | IDENYTPRITQYQCVMEPNQNMRLRTWISKGNQRIPELKKFLRLDNCLEPGVLGTC | 120 | |
| Db | 61 | IDENYTPRITQYQCVMEPNQNMRLRTWISKGNQRIPELKKFLRLDNCLEPGVLGTC | 120 | |
| OY | 121 | ETPNLYYYETDPTDGRNIRENLYVIDTLAASFTQGLGERKKMLTEYREIQLPSKK | 180 | |
| Db | 121 | ETPNLYYYETDPTDGRNIRENLYVIDTLAASFTQGLGERKKMLTEYREIQLPSKK | 180 | |
| OY | 181 | GFYLAFOVGACIALVSVKYYKKCMWITVENLAVDPDITVGSSEFSLVEVHGTCVSSAE | 240 | |
| Db | 181 | GFYLAFOVGACIALVSVKYYKKCMWITVENLAVDPDITVGSSEFSLVEVHGTCVSSAE | 240 | |
| OY | 241 | EAENSPPRHCSAEGSWLPIGKCTKAGYQQXGDPCEPCGRFFYSSSDIQCSCRPTHS | 300 | |
| Db | 241 | EAENAPRHCHCSAEGSWLPIGKCTKAGYQQXGDPCEPCGRFFYSSSDIQCSCRPTHS | 300 | |
| OY | 301 | FSDRGSSRCCEDEYRAPSDDPYVACRPSPASQNIIFNNQTVSLHSPPADNGSR | 360 | |
| Db | 301 | FSDRGSSRCCEDEYRAPSDDPYVACRPSPASQNIIFNNQTVSLHSPPADNGSR | 360 | |
| OY | 361 | NDVYTRILCKKCSMEQGCVPKCSNIGYMPQOTGLEDNVYVIMDLAAHNTFEVEAVNG | 420 | |
| Db | 361 | NDVYTRILCKKCSMEQGCVPKCSNIGYMPQOTGLEDNVYVIMDLAAHNTFEVEAVNG | 420 | |
| OY | 421 | VSDLSRSORLPAVNSITTTGOAAPSOVSGMKERVQORSYQLSWMQPEHPNVIITEYIKY | 480 | |
| Db | 421 | VSDLSRSORLPAVNSITTTGOAAPSOVSGMKERVQORSYQLSWMQPEHPNVIITEYIKY | 480 | |
| OY | 481 | YEKQREKTYSTLTKRSTASINNLKPGVYVYFOIRAYTAAGYNSPPLVYATLEBASG | 540 | |
| Db | 481 | YEKQREKTYSTLTKRSTASINNLKPGVYVYFOIRAFPAAGYNSPPLVYATLEBASG | 540 | |
| OY | 541 | KMFPEATVASSSEONPIIITAVAVAGTIIILVFVFFIIGRRHCGYSKADQ3GDEBLYFH | 599 | |
| Db | 541 | KMFPEATVASSSEONPIIITAVAVAGTIIILVFVFFIIGRRHCGYSKADQ3GDEBLYFH | 599 | |
| RESULT 7 | | | | |
| O8C7N2 | PRELIMINARY; | PRT: | 593 AA. | |
| AC | O8C7N2. | | | |
| DT | 01-MAR-2003 (TREMBLrel. 23, Created) | | | |
| DT | 01-MAR-2003 (TREMBLrel. 23, Last sequence update) | | | |
| DT | 01-MAR-2004 (TREMBLrel. 26, Last annotation update) | | | |
| DE | Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone:G31003G06 product:Eph receptor A7, full insert | | | |
| DE | sequence. | | | |
| GN | Name=EphA7. | | | |
| OS | Mus musculus (Mouse). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | |
| OX | NCBI_TaxID=10090; | | | |
| KN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=C57BL/6J; TISSUE=Hippocampus; | | | |

RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P.; Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Mech. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA The FANTOM Consortium;
 RT the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/Gr.145100;
 RA Carninci P.; Shibata Y.; Hayatsu N.; Sugihara Y.; Shibata K.; Itoh M.;
 RA Kono H.; Okazaki Y.; Muramatsu M.; Hayashizaki Y.;
 RA Suni N.; Ishii Y.; Nakamura S.; Hazama M.; Nishine T.; Harada A.;
 RA Yanamoto R.; Matsuno H.; Sakaguchi S.; Ikegami T.; Kaspiwagi K.;
 RA Fujiwake S.; Inoue K.; Togawa Y.; Izawa M.; Ohara E.; Watahiki M.;
 RA Yoneda Y.; Ishikawa T.; Ozawa K.; Tanaka T.; Matsuura S.; Kawai U.;
 RA Okazaki Y.; Muramatsu M.; Inoue Y.; Kira A.; Hayashizaki Y.;
 RA "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multichannel sequencer.";
 RL Genome Res. 10:1175-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
 RA Adachi J.; Aizawa K.; Akimura T.; Arakawa T.; Bono H.; Carninci P.;
 RA Fukuda S.; Furuo M.; Hanagaki T.; Hara A.; Hashiune W.;
 RA Hayashida K.; Hayatsu N.; Yanamoto K.; Hirooka T.; Hirozane T.;
 RA Hori F.; Imotani K.; Ishii Y.; Itoh M.; Kagawa I.; Kasukawa T.;
 RA Katoh H.; Kawai U.; Kojima Y.; Kondo S.; Kono H.; Kouda M.; Koya S.;
 RA Kurihara K.; Matsuyama T.; Miyazaki A.; Murata M.; Nakamura M.;
 RA Nishi K.; Nomura K.; Numazaki R.; Ohno M.; Ohashi N.; Okazaki Y.;
 RA Saito R.; Satoh H.; Sakai C.; Sakai K.; Sakazume N.; Sano H.;
 RA Sasaki D.; Shibata K.; Shingawa A.; Shiraki T.; Sogabe Y.; Tagami M.;
 RA Tagawa A.; Takahashi F.; Takaku-Akahira S.; Takeda Y.; Tanaka T.;
 RA Tomaru A.; Toyota T.; Yasunishi A.; Muramatsu M.; Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK049848; BAC33955.1; --
 DR HSSP; P54763; 1INX.
 DR WGD; MG1:95276; Epha7.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR001090; Ephrin receptor.
 DR InterPro; IPR003962; FNIII_subd.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR008979; FN blind like.
 DR InterPro; IPR001426; YKase receptorV.
 DR Pfam; PF01404; Ephrin_Ibd_1.
 DR Pfam; PF00041; fn3_1.
 DR PRINTS; PR00014; EPHYRPTII.
 DR ProDom; PD001495; Ephrin_receptor; 1.

DR SMART; SM00615; Eph_1bd; 1.
 DR SMART; SM00060; FN3; 2.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS50853; FN3; 2.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR RECEPTOR.
 KW SEQUENCE 593 AA; 66324 MW; 11980225D73F3D83 CRC64;

Query Match 93.6%; Score 3126; DB 2; Length 593;
 Best Local Similarity 99.7%; Pred. No. 1.9e-225;
 Matches 587; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTGTRPSPWIIILCYIMLGFHNGEQAQAEVLLDSKAQOTLEWISSPPSGMEISG 60
 DB 1 MVTGTRPSPWIIILCYIMLGFHNGEQAQAEVLLDSKAQOTLEWISSPPSGMEISG 60
 QY 61 LDENVTPIRTYQVCQVMEPNONNMLRTNWSKGNQRIFEELKFTLRDQSLPGVLTGCK 120
 DB 61 LDENVTPIRTYQVCQVMEPNONNMLRTNWSKGNQRIFEELKFTLRDQSLPGVLTGCK 120
 QY 121 ETEFLYYETDYGGRNREMLVYKIDTIADESFTQDGLERKMKLNTREIIGPLSKK 180
 DB 121 ETEFLYYETDYGGRNREMLVYKIDTIADESFTQDGLERKMKLNTREIIGPLSKK 180
 QY 181 GFYLAPODVGACIALVSVKYVYKKCWTIVENLAVFPDVTGSEFSLVEVAGTCVSSAE 240
 DB 181 GFYLAPODVGACIALVSVKYVYKKCWTIVENLAVFPDVTGSEFSLVEVAGTCVSSAE 240
 QY 241 EAENSPRMHCSAEGBMWLPICKICIKAGYQOKGDTCEPCGRFPYKSSQDILQCSRPYHS 300
 DB 241 EAENSPRMHCSAEGBMWLPICKICIKAGYQOKGDTCEPCGRFPYKSSQDILQCSRPYHS 300
 QY 301 PSDEGSRCECEGYVAPSDPVACTRPPSAQNIIFINQTVLSLEWSPADNGR 360
 DB 301 PSDEGSRCECEGYVAPSDPVACTRPPSAQNIIFINQTVLSLEWSPADNGR 360
 QY 361 NDVYRILCKKCSWEGECVPCGSNIGYPOQTGLEDDYVYVMDLAHANYTFEYEAANG 420
 DB 361 NDVYRILCKKCSWEGECVPCGSNIGYPOQTGLEDDYVYVMDLAHANYTFEYEAANG 420
 QY 421 VSDLSRSGRLFAAASITTTGAAPSGVSMKEKRVLQRSVOLSWQPEHPNGVITEYEIKY 480
 DB 421 VSDLSRSGRLFAAASITTTGAAPSGVSMKEKRVLQRSVOLSWQPEHPNGVITEYEIKY 480
 QY 481 YEKQRETTYTLTKTSTASINNLKPGTVVYFOIRATTAAGYGVYSPRLDVATLEASG 540
 DB 481 YEKQRETTYTLTKTSTASINNLKPGTVVYFOIRATTAAGYGVYSPRLDVATLEASG 540
 QY 541 KMFEATAVSSSEONPVIIIAVAVAGTIIIVFVFEGFIIGRRHCGYKAD 589
 DB 541 KMFEATAVSSSEONPVIIIAVAVAGTIIIVFVFEGFIIGRRHCGYKAD 589

RESULT 8

EPAT7_CHICK STANDARD; PRT; 993 AA.
 AC 042422;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ephrin type-A receptor 7 precursor (BC 2.7.1.112) (Tyrosine-protein kinase receptor CBP47) (Tyrosine-protein kinase receptor CER11).
 GN Name=EPHA7; Synonyms=CERK11;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=98092111; PubMed=9431814; DOI=10.1016/S0925-4773(97)00147-0;

RA Araujo M., Nieto M.A.;
 RT "The expression of chick EphA7 during segmentation of the central and peripheral nervous system."
 RL Mech. Dev. 68:173-177(1997).
 CC -1- FUNCTION: Receptor for members of the ephrin-A family.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Within the nervous system, expression is restricted to prosomeres 1 and 2 in the diencephalon and all the rhombomeres in the hindbrain during segmentation stages. Later on, a superimposed pattern appears that correlates with the formation of several axonal tracts. In the somitic mesoderm, the expression correlates with segmentation and the guidance of both neural crest and motor axons through the sclerotomes.
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin receptor subfamily.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and all the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; Y14771; CA74643.1; -.
 DR HSSP; P54763; IUPA.
 DR InterPro; IPR006209; EGF_1like.
 DR InterPro; IPR001090; Ephrin_receptor.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-1like.
 DR InterPro; IPR003962; FNIII_subd.
 DR InterPro; IPR008979; Gal_Bind_1like.
 DR InterPro; IPR009030; Gw_fac_recept.
 DR InterPro; IPR011009; Kinase_1like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001660; SAM.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR InterPro; IPR001426; Yase_receptolv.
 DR Pfam; PF01404; Ephrin_1bd; 1.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00069; kinase; 1.
 DR Pfam; PF00536; SAM; 1.
 DR PRINTS; PR00014; FNTYPEIIT.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD001495; Ephrin_receptor; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00615; Eph_1bd; 1.
 DR SMART; SM0060; FN3; 2.
 DR SMART; SM00454; SAM; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS50853; FN3; 2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS50105; SAM_DOMAIN; 1.
 KW ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat; Signal; Transmembrane; Transmembrane; Tyrosine-protein kinase.
 FT SIGNAL 1 30
 FT CHAIN 31 993
 FT DOMAIN 31 551
 FT TRANSMEM 552 572
 FT DOMAIN 573 993
 FT DOMAIN 192 328
 FT DOMAIN 331 433
 FT DOMAIN 443 535
 FT DOMAIN 443 535

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FT DOMAIN 628 889 Protein kinase.
FT 918 982 SAM.
FT SITE 991 993 PDZ-binding motif (Potential).
FT NP_BIND 634 642 ATP (By similarity).
FT DISULFID 74 109 By similarity.
FT BINDING 660 660 ATP (By similarity).
FT ACT_SITE 753 753 By similarity.
FT MOD_RES 603 603 Phosphotyrosine (by autocatalysis)
FT MOD_RES 609 609 Phosphotyrosine (by autocatalysis)
FT MOD_RES 786 786 Phosphotyrosine (by autocatalysis)
FT MOD_RES 935 935 Phosphotyrosine (by autocatalysis)
FT MOD_RES 935 935 Phosphotyrosine (by autocatalysis)
FT CARBOHYD 343 343 N-linked (GlcNAc..) (Potential).
FT CARBOHYD 410 410 N-linked (GlcNAc..) (Potential).
SQ SEQUENCE 993 AA; 111366 MW; EECF9603047608BD CRC64;

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Query Match 90.8%; Score 3031.5; DB 1; Length 593;
Best Local Similarity 94.5%; Pred. No. 4,7e-218;
Matches 566; Conservative 17; Mismatches 11; Indels 5; Gaps 1;

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QY 1 MMYOTRPSMIIICVIMLGPATHTGAQAKEYLLDLSKAQOETELWISSPPSGMEIISG 60
DB 1 MWLSRSLPWPIMICSVMLRPAHGAQAKEYLLDLSKAQOETELWISSPPSGMEIISG 60
QY 1DENYPTIRTYOVCOVMEPNQNMWLRNWSKNAQRIFVELKFTLSDCKSLPGVLGTCK 120
DB 1DENYPTIRTYOVCOVMEPNQNMWLRNWSKNAQRIFVELKFTLSDCKSLPGVLGTCK 120
QY 121ETPNLYYFEDYDGTGRNIRENLYKIDTIADESFTGDIIGERRMKINTVREIGPLSKK 180
DB 121ETPNLYYFEDYDGTGRNIRENLYKIDTIADESFTGDIIGERRMKINTVREIGPLSKK 180
QY 121ETPNLYYFEDYDGTGRNIRENLYKIDTIADESFTGDIIGERRMKINTVREIGPLSKK 180
DB 121ETPNLYYFEDYDGTGRNIRENLYKIDTIADESFTGDIIGERRMKINTVREIGPLSKK 180
QY 181GFYLAPODVACIALYVVKYKKWCMTIVNINAFPTVVGSESSIVKRGCVSSAEE 240
DB 181GFYLAPODVACIALYVVKYKKWCMTIVNINAFPTVVGSESSIVKRGCVSSAEE 240
QY 241EAENSPRMHCSAEGEWLVPIGKICICKAGYQOKGDTCPCCRRFYKSSSOTLQSCRPTHS 300
DB 241EAENSPRMHCSAEGEWLVPIGKICICKAGYQOKGDTCPCCRRFYKSSSOTLQSCRPTHS 300
QY 301FSDPREGSRCECEDGYRAPSDPPYVACTPPSPAPQNLININQTVTSLEWSPADNGGR 360
DB 301FSDPREGSRCECEDGYRAPSDPPYVACTPPSPAPQNLININQTVTSLEWSPADNGGR 360
QY 361NDVTYRILCRCSWEOGECVPCGSGNIGYMPQOQGLDENYTTWMDLAHANVTFEVEAVNG 420
DB 361NDVTYRILCRCSWEOGECVPCGSGNIGYMPQOQGLDENYTTWMDLAHANVTFEVEAVNG 420
QY 421VSDLSRSQRLFAAVSITTTGAAPSOVSGWKKERVLQSRVOLSMQEPHPKGVITTEYIKY 480
DB 421VSDLSRSQRLFAAVSITTTGAAPSOVSGWKKERVLQSRVOLSMQEPHPKGVITTEYIKY 480
QY 481YEKQQRERTYSTLKTSKTSASINNLKPGTYVFOIRAATAAGYGVSPRI DVATLEBASG 540
DB 481YEKQQRERTYSTLKTSKTSASINNLKPGTYVFOIRAATAAGYGVSPRI DVATLEBASG 540
QY 541KMEKATVASEQNVIIIAVAVAGTIIIVFMVFGFTIGRRHCGYSKADLEGDEBELYFH 599
DB 541KMEKATVASEQNVIIIAVAVAGTIIIVFMVFGFTIGRRHCGYSKADLEGDEBELYFH 599

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RESULT 9

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ID 08C276 PRELIMINARY; PRT; 691 AA.
AC 08C276;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Mus musculus 10 days neonate olfactory brain cDNA, RIKEN full-length
DE enriched library, clone:E530015D21 product:Bph receptor A5, full

```

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DE insert sequence.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Komno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Komno H., Akiyama U., Nishi K., Kitesuna T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujisake S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RA Adachi U., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Komno H., Kouda M., Koya S.,
RA Kishira C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohnato N., Okazaki Y.,
RA Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Tova T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK089143; EAC40764.1; -.
DR HSSP; P54763; INDK.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005503; F:G-protein coupled receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0004686; F:protein amino acid phosphorylation; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .; IEA.

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DR InterPro: IPR006209; EGF_l1ke.
DR InterPro: IPR001090; Ephrin_receptor.
DR InterPro: IPR003962; Fcrl1_subd.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR008979; Gal_bind_l1ke.
DR InterPro: IPR009030; Grow_fac_recept.
DR InterPro: IPR001426; Ykase_receptor.
DR Pfam: PF001404; Ephrin_1bd_1.
DR Pfam: PF000041; fn3_2.
DR PRINTS: PR00014; FNTYPEIII.
DR ProDom: PD001495; Ephrin_receptor_1.
DR SMART: SM00615; EPH_1bd_1.
DR SMART: SM00060; FN3_2.
DR PROSITE: PS01186; EGF_2_1.
DR PROSITE: PS50853; FN3_2.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1_1.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2_1.
DR KEGG: K04404; EGF.
SQ SEQUENCE 681 AA; 75336 MW; 92B9187AB78BE722 CRC64;

Query Match 55.7%; Score 1860.5; DB 2; Length 681;
Best Local Similarity 57.1%; Pred. No. 1.5e-130;
Matches 349; Conservative 97; Mismatches 134; Indels 31; Gaps 8;

6 RFPSPWILLCY-----IW-----LLGFATGDAQAKVLLDLSKAQOQTELEWISSPSG 54
25 RVPASLAGCYAPLKGPMITCLLCALRTLLASPSNEVNLIDRTWGDLCWIAFPKNG 84
55 WEIISGLDENTYPIRTYQVCVMEPNQNNMLRTNWSKGNQRIFEVLKFTLRDQNSLPG 114
85 WEIIGEDVENYAPLHTYQVCVMEQNNMLTWSWISNEGASRIFEILKFTLRDQNSLPG 144
115 VLGTCKETPNLYYETDYDTGRNIRENLYKIDITIADESFTELDLGRVKNLTVEYADV 174
145 GLGTCKETPNMYYESPDENGRSISENQYIKIDITIADESFTELDLGRVKNLTVEYADV 204
175 GPLSKKGFYLAFOVAGACIALVSVKVVYKKCKMTIENLAVFPDPTVTESEFSLVEVRGTC 234
205 GPLSKKGFYLAFOVAGACIALVSVKVVYKKCKSVRRHLATFPDPTVTESEFSLVEVRGTC 264
235 VSSAEENENSPRMHCSAEGEMLVPIGKCIKAGYQKGDTCPCGRRRFYKSSSODLQCS 294
265 VN--HSVTDDPRKHKCSAEGEMLVPIGKCMCKAGEEKNGTCQYCRPEGFASPHSOTCS 322
295 RCPHTSSSDRGSSRCCEGDIYRAPSDPYVACTRPPSAQNLIFNINQTVSLIENSP 354
323 KCPHASTHEASTSCVCEKDFFRDSDPPTMACTRPPSAPRNAISNNETSVELEWITP 382
355 ADNGGRDVTYRIICKKCSMEQGEVPCGSNIGVMPOOTGLIEDNYVTYMDLLAHANTFE 414
383 ADTGGRDVTYRIICKKCSNAGVCEEGGCHRYLPOQIGLKNYSVMWVDLLAHANTFE 442
415 VEAVNGVSDLSRSQRLFAAIVITGQAAPQVSGVMKERVLRQSVOLSMQEPHNGVIT 474
443 IEAVNGVSDLSRSQRLFAAIVITGQAAPQVSGVMKERVLRQSVOLSMQEPHNGVIT 502
475 EYEIKYKQREKTYSTLTKTSTASANNLKPGTVYFQIRAYTAAGYGYSPRLDYAT 534
503 EYEIKYKQREKTYSTLTKTSTASANNLKPGTVYFQIRAYTAAGYGYSPRLDYAT 558
535 LEBAISGMKFEAT-----ANSEONPIITIAVAAGTITLVMVNGFIIGRHHGYSKADQ 590
559 -----FETTPVSVASANDSQOPIITIAVSVTVGVILLAVMI-GFLLSGRRCGYSTRKQ 609
591 EGDEE-LYFHS 600
610 DPBEKKHAFHN 620

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AC P54757;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ephrin type-A receptor 5 precursor (EC 2.7.1.112) (Tyrosine-protein
DE kinase receptor EHK-1) (EPH homology kinase-1).
GN Name=EphA5; Synonyms=Ehk-1, Ekh1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_taxid=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4 AND 5).
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=9406777; PubMed=7504232;
RA Maisompierre P.C., Barzenueta N.X., Yancopoulos G.D.;
RT "Ehk-1 and Ehk-2: two novel members of the Ehn receptor-like tyrosine
RT kinase family with distinctive structures and neuronal expression.";
RL Oncogene 8:3277-3288(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 6).
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=95206467; PubMed=7898646; DOI=10.1016/0306-4522(94)90014-0;
RA Taylor V., Miescher G.C., Pfeifer S., Honegger P., Breitschopf H.,
RA Laessmann H., Steck A.U.;
RT "Expression and developmental regulation of Ehk-1, a neuronal Elk-like
RT receptor tyrosine kinase in brain.";
RL Neuroscience 63:163-178(1994).
CC -1- FUNCTION: Receptor for members of the ephrin-A family. Binds to
CC ephrin-A1, -A2, -A3, -A4 and -A5.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: Type I membrane protein.
CC Event=Alternative splicing; Named isoforms=6;
CC Name=1;
CC IsoId=P54757-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P54757-2; Sequence=VSP_003001;
CC Name=3;
CC IsoId=P54757-3; Sequence=VSP_003002;
CC Name=4;
CC IsoId=P54757-4; Sequence=VSP_003003;
CC Name=5;
CC IsoId=P54757-5; Sequence=VSP_003001, VSP_003002, VSP_003003;
CC Name=6;
CC IsoId=P54757-6; Sequence=VSP_003000, VSP_003002;
CC -1- TISSUE SPECIFICITY: Almost exclusively expressed in the nervous
CC system. Predominantly expressed in neurons.
CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin
CC receptor subfamily.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
CC -----
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CC or send an email to license@sib.ch).
CC -----
DR EMBL: X78689; CAAS5357.1; -.
DR PIR: S49015; S49015.
DR PIR: S51603; S51603.
DR HSSP: P54763; 1JPA.
DR InterPro: IPR006209; EGF_l1ke.
DR InterPro: IPR001090; Ephrin_receptor.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR003962; Fcrl1_subd.
DR InterPro: IPR008979; Gal_bind_l1ke.
DR InterPro: IPR009030; Grow_fac_recept.

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DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR001660; SAM.
DR InterPro; IPR001245; Tyr_Kinase.
DR InterPro; IPR008266; Tyr_Kinase_AS.
DR InterPro; IPR001426; YKase_receptorV.
DR Pfam; PF01404; Ephrin_lbd; 1.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00536; SAM; 1.
DR PRINTS; PR00014; FNTYPEIII.
DR PRINTS; PR01009; TYRKINASE.
DR ProDom; PD001495; Ephrin_receptor; 1.
DR ProDom; PD000001; Prot_Kinase; 1.
DR SMART; SM00615; Eph_lbd; 1.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00219; TyrcK; 1.
DR PROSITE; PS01166; EGF_2; UNKNOWN_1.
DR PROSITE; PSS0853; FN3; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PSS0105; SAM_DOMAIN; 1.
KW Alternative splicing; ATP-binding; Glycoprotein; Phosphorylation;
KW Receptor; Repeat; Signal; Transferase; Transmembrane;
KW Tyrosine-protein kinase.
KW SIGNAL 1 26 By similarity.
FT CHAIN 27 1005 Ephrin type-A receptor 5.
FT TRANSMEM 27 575 Extracellular (Potential).
FT DOMAIN 597 1005 Potential.
FT DOMAIN 222 356 Cytoplasmic (Potential).
FT DOMAIN 359 461 Fibronectin type-III 1.
FT DOMAIN 471 561 Fibronectin type-III 2.
FT DOMAIN 677 938 Protein kinase.
FT DOMAIN 967 1005 SAM.
FT NP_BIND 683 691 ATP (By similarity).
FT BINDING 709 709 ATP (By similarity).
FT ACT_SITE 802 802 By similarity.
FT MOD_RES 652 652 Phosphotyrosine (by autocatalysis) (By similarity).
FT MOD_RES 658 658 Phosphotyrosine (by autocatalysis) (By similarity).
FT MOD_RES 835 835 Phosphotyrosine (by autocatalysis) (Potential).
FT MOD_RES 984 984 Phosphotyrosine (by autocatalysis) (By similarity).
FT CARBOHYD 266 266 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 301 301 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 371 371 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 425 425 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 438 438 N-linked (GlcNAc . . .) (Potential).
FT CARBOHYD 463 463 N-linked (GlcNAc . . .) (Potential).
FT VARSPLIC 10 GRRRTGGRGG -> DADGPAQASWCHARR (in isoform 6).
FT VARSPLIC 306 VCRPGFKASPHSGTCKPCPHSYTHEASTSCVCEKDYPR
FT VARSPLIC 357 RESDPRMACT -> G (in isoform 2 and isoform 5).
FT VARSPLIC 358 /FTID=VSP_003001.
FT VARSPLIC 470 RPPAPRNAISNNVETSVFLEWIPPADTGCADVSYIILCK
FT KCSHAGVCEGCGHYVLLQOIGLKTSTVMADPLAHYV
FT TFEIEAVNGVSDLSPTGRVYVAVVTNQA -> T (in isoform 3, isoform 4, isoform 5 and isoform 6).
FT VARSPLIC 597 /FTID=VSP_003002.
FT VARSPLIC 621 SGSCCEGCGRASLCAVAHPSLIW -> R (in isoform 4 and isoform 5).
FT VARSPLIC 621 /FTID=VSP_003003.
FT CONFLICT 170 D -> E (in Ref. 2).
FT CONFLICT 566 G -> A (in Ref. 2).

FT CONFLICT 578 578 G -> A (in Ref. 2).
FT CONFLICT 669 669 G -> A (in Ref. 2).
FT CONFLICT 708 708 T -> I (in Ref. 2).
FT CONFLICT 979 979 T -> I (in Ref. 2).
SQ SEQUENCE 1005 AA; 111007 MW; 1AED42C9693C574 CRC64;
Query Match 54.5%; Score 1819; DB 1; Length 1005;
Best Local Similarity 55.1%; Pred. No. 3,4e-127;
Matches 348; Conservative 96; Mismatches 136; Indels 52; Gaps 10;
QY 6 RPSWIIICV-----IW-----LGFPHGGEQAQKEVLLDLSKQAQTELEWISSPSG 54
DB 25 RVFASLAGCTSAAPLKBPMTCLLLCALRTLLSPSENVLLDSKTVLGDGLIAPFKNG 84
QY 55 WEISGLDENYPTIRTYOVCQVMEPNQNMWLRTNWISKNAQRIFVELKFTLLDQNSLPG 114
DB 85 WEIEIGEDENYAPIHRYOVCQKWEQNMWMLLSWISNBSASPIFELKFTLLDQNSLPG 144
QY 115 VLGTCKETFMVLYYEDYDTGRNIRENLVYKIDITIAADESFTGGDGERMKLNTVEYREI 174
DB 145 GLGTCKETFMVLYYEDDENGKRNIKDQYKIDITIAADESFTLGLDRVMKLNTEYRDV 204
QY 175 GPLSKKGYFLAFODVGACIALVSVKYYKKCWITVENLAVFPPTVGSSESSLVEYRGTC 234
DB 205 GPLSKKGYFLAFODVGACIALVSVRYKKCPVSHLAVFPPTITIGADSSQLLEVSQSC 264
QY 235 VSSAESEAEENSPPMHGSAEGEWLVPIGKICCKAGYOQKDPCEPCGRRFYKSSODLQCS 294
DB 265 VN--HSTVDPRPMHGSABGEMLVPIGKCMCKAGYEENKGTQVCVRGFKASPHSQTCS 322
QY 295 RCTTHFSRDSREGSSRCEDEGYRAPSDPPYVACTRPPAPQVLININOTYLSLEKSP 354
DB 323 KCPHRYTHEASTSCVCEKDYFRRESDEPTTAPPSAPRNAISNVETSVFLEWIP 382
QY 355 ADNGRNDYTYRILYLCRCGSEGEVCPGCSNIGYMOQGLLENYTVMDLLAHAYTFE 414
DB 383 ADTGCGKDVSYIYLCKCKSHAGVCECGHYVLLQOIGLKTSTVMADPLAHNTTFE 442
QY 415 VEAVNGVSDLSRSQRLPAVSIITGQAAPSOYSGVKKERYLQSRVOLSMQEPHNGVIT 474
DB 443 IEAVNGVSDLSPTGRVYVAVVTNQAAPSPVNVKKGAKNISLSLWQEPHNGIIL 502
QY 475 EYIKTYEKDQRRRTYSTLKSTASINNLKGYVYVQIRAVTYAGGNSPRLDVAT 534
DB 503 EYIKTYEKDQ--ETSYTIILKSKETITTAGLKPASVYVQIRARITAGYGVFSRPE--- 558
QY 535 LBEASGKMFEPATV---SSRQNVIIIAVAVAGTIIIVMGVGFII-----GRR- 581
DB 559 -----FETTVFPAASNDQSOPIITIGSVTYGVILLAVMI-GFILSGSCCECGGRAS 609
QY 582 -----HCGYSKADQDEGDEE-LYFHS 600
DB 610 SLCAVAHPSLIWRCYSGKAKQDPEEKMHFN 641
RESULT 11
EPAS_HUMAN STANDARD; PRT; 1037 AA.
AC P54756;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ephrin type-A receptor, 5 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor EHK-1) (Eph homology kinase-1) (Receptor protein-tyrosine kinase HEK7).
DE Name=EPH45; Synonyms=BHK1, HEK7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;

RA Miescher G.C.;
 RL Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.
 RV [2]
 RP SEQUENCE OF 25-1037 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95206782; PubMed=7898931;
 RA Fox G.M., Holcher P.L., Chute H.T., Lindberg R.A., Janssen A.M.,
 BA Baeu R., Wolcher A.A.;
 RT "cDNA cloning and tissue distribution of five human Eph-like receptor
 protein-tyrosine kinases";
 RL Oncogene 10:897-905(1995).
 CC -1 FUNCTION: Receptor for members of the ephrin-A family. Binds to
 CC ephrin-A1, -A2, -A3, -A4 and -A5.
 CC -1 CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1 SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1 ALTERNATIVE PRODUCTS: Type I membrane protein.
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=1;
 CC IsoId=P54756-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P54756-2; Sequence=VSP_002999;
 CC -1 TISSUE SPECIFICITY: Almost exclusively expressed in the nervous
 CC system.
 CC -1 SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin
 CC receptor subfamily.
 CC -1 SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC -----
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 CC -----
 CC EMBL; X95425; CAA64700.1; -;
 DR EMBL; L36644; AAA74245.1; -;
 DR HSSP; P54763; IJPA.
 DR Genew; HGNC:3389; IJPA5.
 DR MIM; 600004; -;
 DR GO; GO:0016021; C:Integral to membrane; TAS.
 DR GO; GO:0005005; F:transmembrane-ephrin receptor activity; TAS.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR001090; Ephrin_receptor.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR003962; FNIII_subd.
 DR InterPro; IPR008979; Gal_bind_like.
 DR InterPro; IPR009030; Grow_fac_recept.
 DR InterPro; IPR011009; Kinase_like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001660; SAM.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR InterPro; IPR001426; Ykase_receptorV.
 DR Pfam; PF01404; Ephrin_lbd; 1.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00069; Kinase; 1.
 DR PRINTS; PR00014; FNTYPEIIT.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRODOM; PD001495; Ephrin_receptor; 1.
 DR PRODOM; PD000001; Prot_kinase; 1.
 DR SMART; SM00615; EPH_lbd; 1.
 DR SMART; SM00060; FN3; 2.
 DR SMART; SM00454; SAM; 1.
 DR SMART; SM00219; TYRK; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS50853; FN3; 2.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS50105; SAM_DOMAIN; 1.
 KW Alternative splicing; ATP-binding; Glycoprotein; Phosphorylation;
 KW Receptor; Repeat; Signal; Transferrase; Transmembrane;
 KW Tyrosine-protein kinase.
 FT SIGNAL 1 24
 FT CHAIN 25 1037 Potential.
 FT DOMAIN 25 573 Ephrin type-A receptor 5.
 FT TRANSMEM 574 594 Extracellular (Potential).
 FT DOMAIN 595 1037 Potential.
 FT DOMAIN 220 354 Cytoplasmic (Potential).
 FT DOMAIN 357 459 Cys-rich.
 FT DOMAIN 469 559 Fibronectin type-III 1.
 FT DOMAIN 675 936 Fibronectin type-II 2.
 FT DOMAIN 965 1029 Protein kinase.
 FT SITE 1035 1037 SAM.
 FT NP_BIND 681 689 PDZ-binding motif (Potential).
 FT BINDING 707 707 ATP (By similarity).
 FT ACT_SITE 800 800 ATP (By similarity).
 FT MOD_RES 650 650 By similarity.
 FT MOD_RES 650 650 Phosphotyrosine (by autocatalysis) (By similarity).
 FT MOD_RES 656 656 Phosphotyrosine (by autocatalysis) (By similarity).
 FT MOD_RES 833 833 Phosphotyrosine (by autocatalysis) (Potential).
 FT MOD_RES 982 982 Phosphotyrosine (by autocatalysis) (By similarity).
 FT CARBOHYD 264 264 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 299 299 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 369 369 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 423 423 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 436 436 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 461 461 N-linked (GlcNAc...) (Potential).
 FT VARSPLIC 597 619 SCCEGCGGRASLCAVNHPIIWM -> R (in isoform 2).
 FT FT
 SQ SEQUENCE 1037 AA; 114784 MW; FC2C46C959A8B699 CRC64,
 Query Match 54.4%; Score 1817; DB 1; Length 1037;
 Best Local Similarity 55.5%; Pred. No. 5e-127;
 Matches 346; Conservative 97; Mismatches 132; Indels 48; Gaps 10;
 QY 6 RPSW--IILCYIWLGFPAHTGEAQAKEVILLDSKAQTELEWISSPSCWEETISGIDE 63
 DB 37 RAPLMTCLILC-----AALRTLLASPSNEVILLDSRTVMGDLGIAPFKNGMEIEGEVDE 91
 QY 64 NYTPIRTYQVQVQVNEPQNNMLPTNMTSKGNAQRIIFVEIKRTLLADCNLSLPGVLGTCKET 123
 DB 92 NYAPLHYQVCKVKEQNNMLTWSISNEGASPIFLKRTLLDCNSLPGLGTCKETP 151
 QY 124 NLVYETDVTGGRNIRENLYKIDITIAADESFTGDLGERKQKNTREIREIGPLSKGIFY 183
 DB 152 NMYTFESPQNGRIKENQYIKIDITIADESFTELDLGRMKNTREIRVDGPILSKGFY 211
 QY 184 LAFQDVGACIALVSVKYYKKCWITVENLAVFPDVTGSEFSSLVVRGTCVSSAAEBEAE 243
 DB 212 LAFQDVGACIALVSVRYKKCPSVRHIAVFPDITIGADSQLLEVSGSCVN--HSVTD 269
 QY 244 NSPRMGSAEGEMLVPIGKCLCKAGYQOKGTCPGCRFRFKSSQDLQGCRCPTHSYSD 303
 DB 270 EPPKMGSAEGEMLVPIGKCMCKAGYEKNGTCVCRGPFKASPHIQSCCKCPHSYTH 329
 QY 304 REGSSRCECEDEGYRAPSDPYVACTRPPAPQNLFININQTVLSLEWSPADNGGRNDV 363
 DB 330 EEAISTCVCCKDYRRRESDEPTMACTRPPAPRAIASVNETSVFLHPIPADTGCRKDV 389
 QY 364 TYRILCRKSWEGECVPCGSNIGYMPQQTGLDENYVTVDLAAHYTBEAVANGVD 423
 DB 390 SYIACKCKNSHAGVCECGGHVRYLPROSGLKNTSVVMVDLLAHYTFEIEAVNGVSD 449

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QY 424 LSSSQRLEFAVSITTGAAAPSOVGVNKKERYLQKRSVOLSKQEPHNPVITEEIKYXK 483
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 450 LSPCARQVSVNVTNQAAPSPTNVKKGKIAKNSILSNQEPDRFGIILEYKIKFEK 509
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 484 DQERRTSTLAKTSTASINNLRKGTYYVQIRAVTAAGNGNSPRLDVATLEBASGMF 543
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 510 DQ-ETSTYTIKSKETTITAGLKPASVYVQIRARITAGYGVFSRPE-----F 557
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 544 EAT---AVSSEONPVIIIAVAAGTIIIVMGVFI-----GRR----- 581
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 558 ETPPVFASSDDSGIPVIANSVTVG-VILLAVIGVLSGSCCECGGRASSLCVAHP 616
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 582 ---HCGYSKADQEGDE-LYFHS 600
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 617 LWRGYSKAKQDPEEKMFHN 639
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

RESULT 12
EPAS_CHICK STANDARD; PRT; 1013 AA.
ID EPAS_CHICK
AC P54755; 007495;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ephrin type-A receptor 5 precursor (EC 2.7.1.112) (Tyrosine-protein
DE kinase receptor CEK7).
GN Name=EPHNA5; Synonyms=CEK7;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Body wall;
RX MEDLINE=95047429; PubMed=7958948; DOI=10.1016/0378-1119(94)90692-0;
RA Sleever D.A., Verderame M.F.;
RT "Identification of a complete Cek7 receptor protein tyrosine kinase
RT coding sequence and cDNAs of alternatively spliced transcripts.";
RL Gene 148:219-226(1994).
RN [2]
RP SEQUENCE OF 512-1013 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93288394; PubMed=8510926;
RA Sajjadi F.G., Pasquale E.B.;
RT "Five novel avian Eph-related tyrosine kinases are differentially
RT expressed.";
RL Oncogene 8:1807-1813(1993).
CC -1- FUNCTION: Receptor for members of the ephrin-A family. Binds to
CC ephrin-A1, -A2, -A3, -A4 and -A5. Able to collapse growth cones.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Comment=Additional isoforms seem to exist;
CC Name=2;
CC IsoId=P54755-1; Sequence=Displayed;
CC Name=1;
CC IsoId=P54755-2; Sequence=VSP_003005;
CC Name=2;
CC IsoId=P54755-3; Sequence=VSP_003004, VSP_003005;
CC -1- TISSUE SPECIFICITY: Detected in the 10-day embryonic brain, weaker
CC expression in the rest of the 10-day embryo. Undetected in adult
CC tissues.
CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin
CC receptor subfamily.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
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CC -----
CC EMBL; U03910; AAB6013.1; -
CC EMBL; U03910; AAB6014.1; -
CC EMBL; U03910; AAB6012.1; -
CC EMBL; Z19058; CAA79508.1; -
CC PIR; I50615; I50615.
CC HSSP; P54763; IUPA.
CC InterPro; IPR006209; EGF-like.
CC InterPro; IPR001090; Ephrin_receptor.
CC InterPro; IPR003961; FN_III.
CC InterPro; IPR008957; FN_III-like.
CC InterPro; IPR003962; FNIII subd.
CC InterPro; IPR008979; Gal_bind-like.
CC InterPro; IPR009030; Grow_fac_recept.
CC InterPro; IPR011009; Kinase-like.
CC InterPro; IPR00719; Prot_kinase.
CC InterPro; IPR001660; SAM_kinase.
CC InterPro; IPR001245; Tyr_kinase.
CC InterPro; IPR008266; Tyr_kinase_AS.
CC InterPro; IPR001426; YKase_receptorV.
CC Pfam; PF01404; Ephrin_1bd; 1.
CC Pfam; PF00041; fn3; 2.
CC Pfam; PF00069; Pkinase; 1.
CC Pfam; PF00516; SAM; 1.
CC PRINTS; PR00014; ENTYPERII.
CC PRINTS; PR00109; TYRKINASE.
CC ProDom; PD001495; Ephrin_receptor; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00615; EPH_1bd; 1.
CC SMART; SM00060; FN3; 2.
CC SMART; SM00454; SAM; 1.
CC SMART; SM00219; TYKc; 1.
CC PROSITE; PS01186; EGF_2; UNKNOWN_1.
CC PROSITE; PS50853; FN3; 2.
CC PROSITE; PS50107; PROTEIN_KINASE_APP; 1.
CC PROSITE; PS50107; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_TYR; 1.
CC PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
CC PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
CC PROSITE; PS50105; SAM_DOMAIN; 1.
CC KW Alternative splicing; ATP-binding; Glycoprotein; Phosphorylation;
CC Receptor; Repeat; Signal; Transferrase; Transmembrane;
CC Tyrosine-protein kinase.
CC SIGNAL 1 31
CC CHAIN 32 1013
CC DOMAIN 32 549
CC TRANSMEM 550 570
CC DOMAIN 571 1013
CC DOMAIN 196 330
CC DOMAIN 333 435
CC DOMAIN 445 535
CC DOMAIN 651 912
CC DOMAIN 941 1013
CC SITE 1011 1013
CC NP_BIND 657 665
CC BINDING 683 683
CC ACT_SITE 776 776
CC MOD_RES 626 626
CC MOD_RES 632 632
CC MOD_RES 809 809
CC MOD_RES 958 958
CC CARBOHYD 240 240
CC CARBOHYD 275 275
CC CARBOHYD 345 345

Potential.
Ephrin type-A receptor 5.
Extracellular (Potential).
Potential.
Cytoplasmic (Potential).
Cys-rich.
Fibronectin type-III 1.
Fibronectin type-III 2.
Protein kinase.
SAM.
PDZ-binding motif (Potential).
APP (by similarity).
APP (by similarity).
By similarity.
Phosphotyrosine (by autocatalysis) (By
similarity).
Phosphotyrosine (by autocatalysis) (By
similarity).
Phosphotyrosine (by autocatalysis) (By
similarity).
Phosphotyrosine (by autocatalysis) (Potential).
Phosphotyrosine (by autocatalysis) (By
similarity).
N-linked (GlcNAc.. ) (Potential).
N-linked (GlcNAc.. ) (Potential).
N-linked (GlcNAc.. ) (Potential).

```


DR GO:0005003; F:ephrin receptor activity; IDA.
 DR InterPro: IPR006209; EGF_1like.
 DR InterPro: IPR001090; Ephrin_receptor.
 DR InterPro: IPR003962; Fcrl1 subd.
 DR InterPro: IPR003961; FN III.
 DR InterPro: IPR008957; FN_III_1like.
 DR InterPro: IPR008979; Gal_Bind_1like.
 DR InterPro: IPR009030; Grow_fac_recept.
 DR InterPro: IPR011009; Kinase_1like.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR001660; SAM_2.
 DR InterPro: IPR011510; SAM_2.
 DR InterPro: IPR001245; Tyr_kinase.
 DR InterPro: IPR008266; Tyr_kinase_AS.
 DR InterPro: IPR001426; Ykase_receptor.
 DR Pfam: PF000414; Ephrin_lbd; 1.
 DR Pfam: PF000414; Efn3_2.
 DR Pfam: PF07647; SAM_2; 1.
 DR PRINTS: PR00014; FNTYPEIIT.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD001495; Ephrin_receptor; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00615; EPH_lbd; 1.
 DR SMART: SM00060; FN3_2.
 DR SMART: SM00454; SAM; 1.
 DR SMART: SM00219; TYKFC; 1.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS00853; FN3_2.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PSS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE: PSS0105; SAM_DOMAIN; 1.
 DR AMP-binding: Glycoprotein; Kinase; Phosphorylation; Receptor;
 KW Transferrase; Transmembrane; Tyrosine-protein kinase
 SQ SEQUENCE 984 AA; 110037 MW; B4CB8101B634D078 CRC64;

Query Match 53.9%; Score 1799; DB 2; Length 984.
 Best Local Similarity 56.8%; Pred. No. 1e-125;

Matches 336; Conservative 103; Mismatches 135; Indels :8; Gaps 7;

QY 13 LCYIMLIG--FAHTGE--NQAKEVILLDSKAQOTLEMTSSPPSMEW::SGLDENYTP 67
 DB 5 LSLVLLGCVLSSGSELSPQPSNEVLLDSKTIQGLGWSYPSHGMEE::SGVDENYTP 64
 QY 68 IRTYQVQWNEPQNMMLRNTNWSISKGAORIPVELKFTLDCNSLPGVLGCKETENLYY 127
 DB 65 IRTYQVQWNEPQNMMLRNTNWSISKGAORIPVELKFTLDCNSLPGVLGCKETENLYY 124
 QY 128 YETDYDTGRNIRENTLYVKIDTIADESFTQDGERKKKINTEVREIGPL3KKGFYLAFO 187
 DB 125 MESDDHGVAFREHQFRTKIDTIADESFQMDGDRILKINTEIREVGVYKKGFIYAFQ 184
 QY 188 DVGACIALVSVKYYKKCGMTIVENLAVFPDTVTGSESSSLVEVRGTQVSS4EEEAENSPR 247
 DB 185 DVGACIALVSVRYVFKKCPFTVKIAMFPDTPV-MDSQSLVEVRGSCVNN3SK3--EDPPR 241
 QY 248 MHGSAEGEMVLPISGKICCKAGYQOKGDTCPGCGRPFKSSQDLQGRCCTHSPSDEGS 307
 DB 242 MYGSTESEMLVPIGKCTCANAGYERGRFICQACRPGFKASDGAACKCKCPHSTQDGS 301
 QY 308 SRCECEDGYRASPDPYVACTRPPAPONLIFINQITVSLSESPADN3GRNDVYR1 367
 DB 302 MNCRCENNVYRAEKDPPSMACTRPPSPARVVISNINETSVLDMSPWLDTGKRDITFNI 361
 QY 368 LCKRCSEGECEVCPGCSNIGMPQOTLENDYTTWDLMLHANTFEVEVNGVSDLSRS 427
 DB 362 ICKKCGNNVQCEPCSPNVRFPLROLGLTNTTYVVDLALHTYTFEIDVNVGSELSSP 421
 QY 428 QRLFAVSIITGGAAPSOVSGWMEKRYLQSVOLSWOEPHPGVITREYIKYKXKORE 487
 DB 422 PROJAAVSITTNQAPSPVMTIKDRTSRNSISLSWQEPHPHPIIDYIEVKYKXKORE 481

QY 488 RYVSLTKSTSTASINNLRGTYVYFOIRAPVAGYNSPRLDVATLEBASGMEEATA 547
 DB 482 TSYTLIRAGTNTVITSLKPDITYVFOIRAPVAGYNSRKREFTSP-----DSFS 534
 QY 548 VSESQNPVILLNVAVAGTIIIVFWPFGFLIRHCGYKADQEGEE-LYF 598
 DB 535 ISGENSHVMAISAAVAIVLT--VVTYVLVGRFGYHKSRSASAEKRLHF 584
 RESULT 14
 ID EPA3_HUMAN STANDARD; PRT; 983 AA.
 AC P29320; Q9H2V3; Q9H2V4; Created
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Ephrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor ETK1) (HEK4).
 GN Name=EPHA3; Synonyms=ETK, ETK1, HEK;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=92179233; PubMed=1311845;
 RA Wicks I.P., Wilkinson D., Salvaris E., Boyd A.W.;
 RT "Molecular cloning of HEK, the gene encoding a receptor tyrosine kinase expressed by human lymphoid tumor cell lines";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:1611-1615 (1992).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=20441582; PubMed=10987298;
 RA Chiari R., Hames G., Stroobant V., Texier C., Maille B., Boon T., Coulle P.G.;
 RT "Identification of a tumor-specific shared antigen derived from an Eph receptor and presented to CD4 T cells on HLA class II molecules";
 RL Cancer Res. 60:4855-4863 (2000).
 RN [3]
 RP SEQUENCE OF 21-29 AND 840-860, AND CHARACTERIZATION.
 RX MEDLINE=9217681; PubMed=1737782;
 RA Boyd A.W., Ward L.D., Wicks I.P., Simpson R.J., Salvaris E., Wilks A., Welch K., Loudovaris M., Rockman S., Busnals I.;
 RT "Isolation and characterization of a novel receptor-tye protein tyrosine kinase (hek) from a human pre-B cell line.";
 RL J. Biol. Chem. 267:3262-3267 (1992).
 RN [4]
 RP SPICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).
 RX PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
 RA Hillman R.T., Green R.E., Brenner S.E.;
 RT "An unappreciated role for RNA surveillance";
 RL Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).
 CC - FUNCTION: Receptor for members of the ephrin-A family. Binds to ephrin-A2, -A3, -A4 and -A5. Could play a role in lymphoid function.
 CC - CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
 CC - SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).
 CC - Secreted (isoform 2).
 CC - ALTERNATIVE PRODUCTS:
 CC - Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P29320-1; Sequence=displayed;
 CC Note=May be produced at very low levels due to a premature stop codon in the mRNA, leading to nonsense-mediated mRNA decay;
 CC Name=2;
 CC IsoId=P29320-2; Sequence=VSP_002995, VSP_002996;
 CC - TISSUE SPECIFICITY: Widely expressed. Highest level in placenta.
 CC - SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin receptor subfamily.
 CC - SIMILARITY: Contains 2 fibronectin type III domains.

CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M83941; AAA58633.1; -;
 DR EMBL; AF213459; AAG3576.1; -;
 DR EMBL; AF213460; AAG3577.1; -;
 DR EMBL; A28003; CA01906.1; -;
 DR PIR; A38224; A38224;
 DR HSSP; P54763; 1JPA;
 DR Genew; HGNC:3387; EPHA3.
 DR MIM; 179611; -;
 DR GO; GO:0005887; C:Integral to plasma membrane; TAS.
 DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR001090; Ephrin_receptor.
 DR InterPro; IPR003961; FN III.
 DR InterPro; IPR003957; FN III-like.
 DR InterPro; IPR003962; FcII subd.
 DR InterPro; IPR008979; Gal bind like.
 DR InterPro; IPR009030; Grow_fac_recept.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001660; SAM.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR InterPro; IPR001426; Ykase_receptor.
 DR Pfam; PF01404; Ephrin_Lbd; 1.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF00536; SAM; 1.
 DR PRINTS; PR00014; FNTYPEIII.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD001495; Ephrin_receptor; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS05853; FN3_2.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS50105; SAM DOMAIN; 1.
 KM Alternative splicing; ATP-binding; Direct protein sequencing;
 KM Glycoprotein; Phosphorylation; Receptor; Repeat; Signal; Transferase;
 KM Transmembrane; Tyrosine-protein kinase.
 FT SIGNAL 1 20
 FT CHAIN 21 983
 FT DOMAIN 21 541
 FT TRANSMEM 542 565
 FT DOMAIN 566 983
 FT DOMAIN 189 322
 FT DOMAIN 325 429
 FT DOMAIN 437 528
 FT DOMAIN 621 882
 FT DOMAIN 911 975
 FT SITE 981 983
 FT NP_BIND 627 635
 FT BINDING 653 653
 FT ACT_SITE 746 746
 FT MOD_RES 596 596
 FT MOD_RES 602 602
 FT MOD_RES 779 779

FT CARBOHYD 232 232 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 337 337 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 391 391 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 404 404 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 493 493 N-linked (GlcNAc. . .) (Potential).
 FT VASPLIC 532 539 SFSISGS -> CWYFNAAV (in isoform 2).
 FT VASPLIC 540 983 /Ftrid=VSP_002995.
 FT VASPLIC 540 983 Missing (in isoform 2).
 FT CONFLICT 507 507 F -> L (in Ref. 1; CA01906).
 FT CONFLICT 724 724 V -> L (in Ref. 1; CA01906).
 FT CONFLICT 911 911 S -> T (in Ref. 2).
 FT CONFLICT 924 924 R -> W (in Ref. 2).
 SO SEQUENCE 983 AA; 110086 MW; B8D900FA80FF5121 CRC64;
 Query Match 53.8%; Score 1796; DB 1; Length 983;
 Best Local Similarity 57.6%; Pred. No. 1,7e-125;
 Matches 329; Conservative 102; Mismatches 128; Indels 12; Gaps 5;
 QY 28 QAAKEVLLDSKQAQTELEWISSPPSGMEISGLDENYTPRTYQVCQVNEPNNQMLRT 87
 DB 25 QPSNEVULLDSKTIQSELGMIISYSHGMBEISGVDEHTPTRTYQVCNMDHSONMLRT 84
 QY 88 NMISGNAORIFVBLKFTLRDONSIPVLTGCKETFMILYYETDYGRIRENLVYKID 147
 DB 85 NMVPRNSAQKIYVBLKFTLRDONSIPVLTGCKETFMILYYESDDHGVKREHQFKID 144
 QY 148 TIADSEFTQDGLGERCKKANTEVREIGPLSKKPYLAFQDVACIALYVSKYVKKCWT 207
 DB 145 TIADSEFTQDGLDRILKNTKTEIREVGPNVKKPYLAFQDVACIALYVSKYVKKCP 204
 QY 208 IVENTLAVFPPTVTSSEPSLVEVGTGCVSAEAEENSPRHCSAEGEMLVPIGKICKA 267
 DB 205 TVKNLAFPPDTP-MDSQSLVEVSGCVNNSKE--EPPRYVCTBGBMLVPIGKICNA 261
 QY 268 GYQKQDTCPECGRPFYKSSSODLQCSRPTSPSDESGRCECDGYRAPSPDPVYA 327
 DB 262 GYERGFMCQACRGFFKALDGNMKCAKCPHSGTQSDGNNCKENNYFPADDPSPMA 321
 QY 328 CTRPPSAPONLIIFINQTTVLSLESPADNGGRNDVYTRILCKRCSGEQECVCGSNIG 387
 DB 322 CTRPPSPRRVVISININETSVLDMSPDLTGGRVDVFNNIIKKCKGNMKICGECSPVR 381
 QY 388 YMPQQTGLENDYVYVWMLLAHANTFEVAVNGVSDLSRSORLPAVASITGOAAPSOVS 447
 DB 382 FLPRQGLITVTVTLAHTNTEFEIDAVNGVSELSPPROPAVASITNOAAPSPVL 441
 QY 448 GVMKERYLQRSVOLSWQEPHPNGVITEIKYKQDQRETYSTLTKTSASINNLKP 507
 DB 442 TIKDRTSRNSISLSWQEPHPNGIILDYEVKYEKQEQESTYITLARGTNVTISLKP 501
 QY 508 GTTVVFOIRAVTAAGYNGYBRDLVATLEASGCMFATAVSSQNPVIITAAVAVAGTI 567
 DB 502 DTIVVFOIRAVTAAGYNGYBRDLVATLEASGCMFATAVSSQNPVIITAAVAVAGTI 567
 QY 568 ILVFWVFGFIIRHGHGYSKADQGDDELYE 598
 DB 555 LITVIVY-VLIG-RFCGYKSKGADKRLHF 583
 RESULT 15
 ID Q6P4R6 PRELIMINARY; PRT; 983 AA.
 AC Q6P4R6;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE EPHA3 protein.
 OS Homo sapiens (Human).
 CC Eukaryota; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Euteleostomi; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_Taxid=9606;
 RN [1]

RA SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strassberg R.L., Collins G.D., Grosse L.H., Deize J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Aleschul S.F., Zeeberg B., Butlov K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Mac S.I., Wang J., Hsieh ?
 RA Ditschenko L., Marinina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stepien W., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratna P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.3.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
 RA Jones S.U., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Strassberg R.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 CC -1 CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1 SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1 SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin
 CC receptor subfamily.
 DR EMBL; BC063282; AAH63282.1; -
 DR HSSP; P54763; 1KGY.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0005003; F:ephrin receptor activity; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006458; P:protein amino acid phosphorylation; IEA.
 DR GO; GO:0007169; P:transmembrane receptor protein tyrosine k.n. .; IEA
 DR InterPro: IPR006209; EGF like.
 DR InterPro: IPR001090; Ephrin receptor.
 DR InterPro: IPR003962; Fcili subd.
 DR InterPro: IPR003961; FN_III-like.
 DR InterPro: IPR008957; FN_III-like.
 DR InterPro: IPR008979; Gal bind like.
 DR InterPro: IPR011009; Kinase like.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR001660; SAM.
 DR InterPro: IPR011510; SAM_2.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR InterPro: IPR008266; Tyr_kinase AS.
 DR InterPro: IPR001426; YKase receptorV.
 DR Pfam; PF00044; Ephrin_lbd_1.
 DR Pfam; PF00041; fn3_2.
 DR Pfam; PF07647; SAM_2; 1.
 DR PRINTS; PR00014; FNTYPRIT1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD0001495; Ephrin receptor; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00615; EPH_lbd; 1.
 DR SMART; SM00060; FN3_2.
 DR SMART; SM00454; SAM; 1.
 DR SMART; SM00220; S_TKC; 1.
 DR SMART; SM00219; TYRKc; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS00853; FN3_2.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.

DR PROSITE, PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE, PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE, PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE, PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE, PS50105; SAM_DOMAIN; 1.
KW ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;
KW Transferrase; Transmembrane; Tyrosine-protein kinase.
SQ SEQUENCE 963 AA; 110160 MW; 1EBDABFC59282527 CRC64;

Query Match 53.8%; Score 1796; DB 2; Length 983;
Best Local Similarity -57.6%; Pred. No. 1.7e-125;
Matches 329; Conservative 102; Mismatches 128; Indels 12; Gaps 5;

28 QAAKEVLLDSKAQQTELEWISSPPSGWEEISGLDENTYPIRTYQVCQVMEPNQNNWLRT 87

| QUESTION | ANSWER |
|--------------------------------------|--|
| 1. What is the purpose of the study? | To determine the effect of the use of a mobile phone on the performance of a simulated driving task. |
| 2. What is the research hypothesis? | It is hypothesized that the use of a mobile phone will result in a decrease in performance on a simulated driving task. |
| 3. What is the independent variable? | The independent variable is the use of a mobile phone, which is manipulated into two conditions: 'no phone' and 'phone use'. |
| 4. What is the dependent variable? | The dependent variable is the performance on a simulated driving task, which is measured by the number of errors made and the time taken to complete the task. |
| 5. What is the experimental design? | The experimental design is a between-subjects design, where participants are randomly assigned to either the 'no phone' or 'phone use' condition. |
| 6. What are the participants? | The participants are 20 young adults, aged between 18 and 25, who are experienced drivers and have no history of alcohol or drug use. |
| 7. What are the procedures? | The procedures involve a pre-test to familiarize participants with the driving task, followed by two trials of the driving task. In the first trial, participants are in the 'no phone' condition, and in the second trial, they are in the 'phone use' condition. The driving task involves navigating a simulated road with various obstacles and traffic. |
| 8. What are the results? | The results show that participants in the 'phone use' condition made significantly more errors and took significantly longer to complete the driving task compared to participants in the 'no phone' condition. |
| 9. What are the conclusions? | The conclusions are that the use of a mobile phone significantly impairs performance on a simulated driving task, and therefore, it is recommended that drivers should avoid using a mobile phone while driving. |

Db 85 NWVPRNSAOKIYVELKFTLRDCNSIPLVLGTCKETFNLYMESDDDHGVKFRFHQFTKID 144

QY 148 TIADESFQGDIGERKMLNTEVREIGPLSKGFIYAFQDVGACIALVSVKYYKKCW 207

Db 145 TIADESFTQMDLGRILKLTNTETIREVGPVKKGFYLAFDQDVGACVALSVRVYFKKCPF 204

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067 |::|::| : |||||::|::| |::|::| |  
068 |::|::|::| : |||||::|::| |::|::| |
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268 GYQKGDTCPCGRFYKSSQDLQCSRCPTHSFSDREGSSRCECEDGYRAPSDPPYA 327

Db 262 GYERGFMCQCRPGFYKALDGNMKCAKCPHSSSTQEDGSMNCRCENNYFRADKDP SMA 321

328 CIRPSSAPQNLIFNINQIIVSLEWSPPADNGKNDVIKILDLKRCSEWEGELVFCSSNIG 50/

388 YMBDCTCI EDNYITWMDLI AHANYTEEEVAIVNGVSDI SPSQPI.FAAYSTTTCGAAPSQVS 447

Db 382 FLPRQFGLTNTVTVDLLAHTNTYTFEIDA VNGVSELSPPRQFAVSIITNQAPSPVL 441

QY 448 GVMKEVLQRSVQLSWEPEHPNGVITEYEIKYKEDQRERTYSTLTKSTASINNLKP 507

74 11NDN10NNS10J00M02EFENHNG11DD1EVAN1ENKED10111UNH10N1N11100NE 204

Db 502 DTLYFOIRARTAGYGTNSRKEFEETSP-----DSFSISGESSOVMIASAVAVII 554

QY 568 ILVEMVEGFIIGRRHCGYSKADQEGDEEL,YF 598

Db 555 LITVVIY-VLIG-RFCGYSKSKHGADKRLHF 583

Search completed: August 23, 2005, 08:30:06

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: August 23, 2005, 08:26:40 ; Search time 16.7136 Seconds

(without alignments)
3603.755 Million cell updates/sec

Title: US-10-073-064-5

Sequence: 1 MVQTRPPSWILLCYWLLG.....DMEKTOHKKMMIASCSRL 626

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR.79:.*
2: PIR1.*
3: PIR2.*
4: PIR3.*
5: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|----------|--------------------|
| 1 | 3338 | 100.0 | 626 | 2 148614 | developmental kina |
| 2 | 3199 | 95.8 | 610 | 2 148612 | developmental kina |
| 3 | 3191 | 95.6 | 998 | 2 JC5672 | receptor tyrosine |
| 4 | 3159.5 | 94.7 | 605 | 2 JC5673 | receptor tyrosine |
| 5 | 3139 | 94.0 | 998 | 2 I58351 | receptor tyrosine |
| 6 | 1841 | 55.2 | 991 | 2 178843 | receptor protein-t |
| 7 | 1834 | 54.9 | 981 | 2 S51604 | receptor-like tyro |
| 8 | 1819 | 54.5 | 1005 | 2 S49015 | receptor tyrosine |
| 9 | 1800 | 53.9 | 1013 | 2 I50615 | receptor-type prot |
| 10 | 1796 | 53.8 | 983 | 2 A38224 | protein-tyrosine k |
| 11 | 1790.5 | 53.6 | 985 | 2 I51549 | receptor tyrosine |
| 12 | 1783.5 | 53.4 | 983 | 2 B45583 | receptor tyrosine |
| 13 | 1783.5 | 53.4 | 983 | 2 A45583 | receptor tyrosine |
| 14 | 1741.5 | 52.2 | 986 | 2 178844 | receptor protein-t |
| 15 | 1723 | 51.6 | 986 | 2 S78059 | protein-tyrosine k |
| 16 | 1655 | 49.6 | 948 | 2 S51605 | receptor-like tyro |
| 17 | 1498 | 44.9 | 995 | 2 A56599 | embryo kinase 5 - |
| 18 | 1467.5 | 44.0 | 970 | 2 178842 | receptor protein-t |
| 19 | 1449 | 43.4 | 984 | 2 A39753 | protein-tyrosine k |
| 20 | 1398 | 41.9 | 898 | 2 S47489 | receptor tyrosine |
| 21 | 1390 | 41.6 | 893 | 2 S51603 | receptor-like tyro |
| 22 | 1348 | 40.4 | 885 | 2 I51672 | receptor tyrosine |
| 23 | 1335 | 40.0 | 849 | 2 I50617 | protein-tyrosine k |
| 24 | 1276 | 38.2 | 988 | 2 I50611 | protein-tyrosine k |
| 25 | 1273.5 | 38.2 | 952 | 2 S37627 | protein-tyrosine k |
| 26 | 1269.5 | 38.0 | 952 | 2 I50612 | protein-tyrosine k |
| 27 | 1257 | 37.7 | 993 | 2 148653 | mouse developmenta |
| 28 | 1248.5 | 37.4 | 976 | 2 A36355 | protein-tyrosine k |
| 29 | 1231.5 | 36.9 | 877 | 2 148967 | brain-specific kin |

| | | | | | |
|----|--------|------|------|----------|--------------------|
| 30 | 1199.5 | 35.9 | 977 | 2 S49004 | tyrosine kinase Mp |
| 31 | 1169 | 35.0 | 938 | 2 149071 | protein kinase - m |
| 32 | 1139.5 | 34.1 | 975 | 2 148974 | receptor-protein t |
| 33 | 1072.5 | 32.1 | 1006 | 2 JC5526 | kinase-defective E |
| 34 | 1064.5 | 31.9 | 984 | 2 A34076 | protein-tyrosine k |
| 35 | 1035.5 | 31.0 | 987 | 2 148652 | mouse developmenta |
| 36 | 1034 | 31.0 | 987 | 2 A54092 | protein-tyrosine k |
| 37 | 1022.5 | 30.6 | 987 | 2 148953 | eph-related recept |
| 38 | 784 | 23.5 | 1019 | 2 T13039 | tyrosine kinase re |
| 39 | 544 | 16.3 | 1122 | 2 T42400 | Fbh receptor tyros |
| 40 | 382.5 | 11.5 | 919 | 2 T29581 | hypothetical prote |
| 41 | 362 | 10.8 | 612 | 2 S33506 | protein-tyrosine k |
| 42 | 251 | 7.5 | 87 | 2 C45583 | receptor tyrosine |
| 43 | 215.5 | 6.5 | 1232 | 2 T43027 | neural cell adhesi |
| 44 | 209 | 6.3 | 1436 | 2 JC5290 | protein-tyrosine-p |
| 45 | 206.5 | 6.2 | 1825 | 2 C88400 | protein H19M22.1 l |

ALIGNMENTS

| | | | |
|----|-----|---|-----|
| QY | 1 | MVQTRPPSWILLCYWLLGFAHTGEAQAQAVLLDSKAQOTLEWISSPPSGMEISG | 60 |
| DB | 1 | MVQTRPPSWILLCYWLLGFAHTGEAQAQAVLLDSKAQOTLEWISSPPSGMEISG | 60 |
| QY | 61 | LDENYTPIRTYQVQVMEPNQNMWLRNWSKGAQRIPELKTLLDQNSLPGVLTGCK | 120 |
| DB | 61 | LDENYTPIRTYQVQVMEPNQNMWLRNWSKGAQRIPELKTLLDQNSLPGVLTGCK | 120 |
| QY | 121 | ETFWLYYETDYGGRNIRENLVYKIDTIADESFTQGDGERKMKLNTREIIGPLSKK | 180 |
| DB | 121 | ETFWLYYETDYGGRNIRENLVYKIDTIADESFTQGDGERKMKLNTREIIGPLSKK | 180 |
| QY | 181 | GFYLAPODVAGACIALVSKVYKKKWTIVENLAVFPDTVTSBPSLVEVGTGVSSAE | 240 |
| DB | 181 | GFYLAPODVAGACIALVSKVYKKKWTIVENLAVFPDTVTSBPSLVEVGTGVSSAE | 240 |
| QY | 241 | EAENSPPMHGSAESEMVLPIGKCIQKAGYQKGTCEPCGRRFYKSSQDLOCSRCPHHS | 300 |
| DB | 241 | EAENSPPMHGSAESEMVLPIGKCIQKAGYQKGTCEPCGRRFYKSSQDLOCSRCPHHS | 300 |
| QY | 301 | FSDEGSSRCCEGCVYRAPSDPYVACTRPPSAPOULIFINQITVLSLEMSPPADNGR | 360 |
| DB | 301 | FSDEGSSRCCEGCVYRAPSDPYVACTRPPSAPOULIFINQITVLSLEMSPPADNGR | 360 |
| QY | 361 | NDVTYRILCKKCSWQECVPCGSGNIGMPQOTGLENNYVTVMDLLAHANTFEVAVNG | 420 |
| DB | 361 | NDVTYRILCKKCSWQECVPCGSGNIGMPQOTGLENNYVTVMDLLAHANTFEVAVNG | 420 |
| QY | 421 | VSDLSRQRLFAANSITTTGAAPSOVGVWKEKRVLOQSNQEPHPNVTITEYELKY | 480 |
| DB | 421 | VSDLSRQRLFAANSITTTGAAPSOVGVWKEKRVLOQSNQEPHPNVTITEYELKY | 480 |

| | | |
|-----------|---|-----|
| OY | 481 YEKDQERYSTLKTSTASINNLKPGVYVFQIRATTAAGYGNYSRLLVATLEBASG | 540 |
| Db | 481 YEKDQERRYSTLTKTSTASINNKLPGTVYFQIRATAAGYGNYSRLLVATLEBASG | 540 |
| OY | 541 KMEEATAVASEQNPIVIIIVVAAGTILVEMFGIIGRRHCGSKADQZGDELYFHS | 600 |
| Db | 541 KMEEATAVASEQNPIVIIIVVAAGTILLVEMFGIIGRRHCGSKADQZGDELYFHS | 600 |
| OY | 601 LYREGDGMEKTOHNKKMMIASCSRL | 626 |
| Db | 601 LYREGDGMEKTOHNKKMMIASCSRL | 626 |

RESULT 2
I48612
developmental kinase 1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I48612; S51741
R:Ciossek, T.; Millaer, B.; Ullrich, A.
Oncogene 9, 97-108, 1995
A:Title: Identification of alternatively spliced mRNA encoding variants of MDX1, a novel
A:Reference number: I48611
A:Accession: I48612
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-610 <RES>
A:Cross-references: UNIPROT:Q61772; EMBL:X79083; NID:g607135; P1DN:CAAS5688.1; PID:g607171

| | | | | |
|---------------------------|---------|---------------------|-----------|-------------|
| Query Match | 95.8%; | Score 3199; | DB 2; | Length 610; |
| Best Local Similarity | 100.0%; | Pred. No. 6.6e-223; | | |
| Matches 601; Conservative | 0; | Mismatches 0; | Indels 0; | Gaps 0; |

| | | | |
|----|-----|--|-----|
| QY | 1 | MVQTRPSPSWIILCYIMLGFAPHTGEAOAAEVLILDSKAOQTLEWISSPSSMEIISG | 60 |
| Db | 1 | MVQTRPSPSWIILCYIMLGFAPHTGEAOAAEVLILDSKAOQTLEWISSPSSMEIISG | 60 |
| QY | 61 | LDENYTPIRTYQVCQWMEPNQNNMLRTNWSISKGAORIFVELKFTLLDCNSLPGVLGTCK | 120 |
| Db | 61 | LDENYTPIRTYQVCQWMEPNQNNMLRTNWSISKGAORIFVELKFTLLDCNSLPGVLGTCK | 120 |
| QY | 121 | ETFMLYYYEEDDYDGRNIRENLYKIKITIADESFQTGDLGERCKKNTEREIGPLSK | 180 |
| Db | 121 | ETFMLYYYEEDDYDGRNIRENLYKIKITIADESFQTGDLGERCKKNTEREIGPLSK | 180 |
| QY | 181 | GFYLAPODVGACIALVSVKYVKKCWITIVENLAFAFPDVTGSESSSLVEYRGTCVSSAE | 240 |
| Db | 181 | GFYLAPODVGACIALVSVKYVKKCWITIVENLAFAFPDVTGSESSSLVEYRGTCVSSAE | 240 |
| QY | 241 | EAENSPRMHCAGEEMLVPIGKCICKAGYQKGDTCBPCGRFPYKSSSODLQCRPTH | 300 |
| Db | 241 | EAENSPRMHCAGEEMLVPIGKCICKAGYQKGDTCBPCGRFPYKSSSODLQCRPTH | 300 |
| QY | 301 | FSDREGSSRCCEGCTYRAPSDPYVACTRPSPAPNULFININOTYTSLEWSPADNGR | 360 |
| Db | 301 | FSDREGSSRCCEGCTYRAPSDPYVACTRPSPAPNULFININOTYTSLEWSPADNGR | 360 |
| QY | 361 | NDVYRYILCKRCSMEOGECVPCGSNIGYMPQOTGLEDNYVTVMMLLHAAYTFEVAWNG | 420 |
| Db | 361 | NDVYRYILCKRCSMEOGECVPCGSNIGYMPQOTGLEDNYVTVMMLLHAAYTFEVAWNG | 420 |
| QY | 421 | VSDLSRSQRLEPAAVSITTTGQAPSPQVSGVMKERVLOBSVOLSWQEPHPNVITREYIKY | 480 |
| Db | 421 | VSDLSRSQRLEPAAVSITTTGQAPSPQVSGVMKERVLOBSVOLSWQEPHPNVITREYIKY | 480 |
| QY | 481 | YEKQQRERTYSTLTKTSTASINNLKRGTYVVPQIRAVTAAGYGNYPRLDVALLEBASG | 540 |
| Db | 481 | YEKQQRERTYSTLTKTSTASINNLKRGTYVVPQIRAVTAAGYGNYPRLDVALLEBASG | 540 |
| QY | 541 | KMFPEATVSSQONPVIIIAVAVAGTIIILVMVNGFIIIGRHGCGYADCEGDELELYHS | 600 |
| Db | 541 | KMFPEATVSSQONPVIIIAVAVAGTIIILVMVNGFIIIGRHGCGYADCEGDELELYHS | 600 |

QY 601 L 601
Db 601 L 601

RESULT 3
JC5672
receptor tyrosine kinase (EC 2.7.-.-) Etk precursor - mouse

C>Date: 20-Nov-1997 #sequence revision 20-Nov-1997 #text_change 09-Jul-2004
C:Accession: JCS672; 148611; S51740
R:Talukder, A.H.; Muramatsu, T.; Kaneda, N.
Cell Struct. Punct. 22, 477-485, 1997
A>Title: A novel truncated variant form of Etk/MDK1 receptor tyrosine kinase is expressed
A:Reference number: JCS672; MUID:98035156; PMID:9368721

A:Title: Identification of alternatively spliced mRNA encoding variants of MDK1, a novel
A:Reference number: 148611
A:Accession: 148611
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-998 <RES>

A:Cross-references: EMBL:JX79082; NID:9607133; PID:CAAS5687.1; PID:9607134
C:Comment: This enzyme plays a role during development involving differentiation and proliferation
C:Superfamily: protein-tyrosine kinase, receptor type eph, fibronectin type III repeat homology
C:Keywords: ATP; brain; phosphotransferase; transmembrane protein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:331-998/Product: receptor tyrosine kinase Etk #status predicted <MAT>
F:331-553/Domain: extracellular #status predicted <EXT>
F:331-438/Domain: fibronectin type III repeat <FN1>
F:441-534/Domain: fibronectin type III repeat <FN2>
F:554-579/Domain: transmembrane #status predicted <TM>
F:631-897/Domain: protein kinase homology <KIN>
F:639-647/Region: protein kinase ATP-binding motif
F:920-966/Domain: SAM homology <SAM>

| | | | | |
|-----------------------|-----------------|---------------------|-----------|-------------|
| Query Match | 95.6% | Score 3191; | DB 2; | Length 998; |
| Best Local Similarity | 100.0% | Pred. No. 4.8e-222; | | |
| Matches 599; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |

| | | | |
|----|-----|---|-----|
| Qy | 1 | MVQVTRPSPWIIICXIMLGFPAHFGEMOAAEVLILSKAOQTELEWISSPSSGMEETSG | 60 |
| Db | 1 | MVQVTRPSPWIIICXIMLGFPAHFGEMOAAEVLILSKAOQTELEWISSPSSGMEETSG | 60 |
| Qy | 61 | LDENYTPIRTYQVCQVMEPNQNNMLRTWMSKGNAPRIFEVLKFTLRDQNSLPGLVGTCK | 120 |
| Db | 61 | LDENYTPIRTYQVCQVMEPNQNNMLRTWMSKGNAPRIFEVLKFTLRDQNSLPGLVGTCK | 120 |
| Qy | 121 | ETPNLYYYEYTDYDGRNIRENLYXKIDTPIADESFTQSDJGERMKXKNTVEIREJGPLSKK | 180 |
| Db | 121 | ETPNLYYYEYTDYDGRNIRENLYXKIDTPIADESFTQSDJGERMKXKNTVEIREJGPLSKK | 180 |
| Qy | 181 | GFYLAFOQVACIALVSXKYVKKCMTIIVENLAJFPPDVTGSEFSSLYEVRGTCVSSAAE | 240 |
| Db | 181 | GFYLAFOQVACIALVSXKYVKKCMTIIVENLAJFPPDVTGSEFSSLYEVRGTCVSSAAE | 240 |
| Qy | 241 | EAENSPPMHGCAABEEMLVPTGKCI CKAGXQCKGPTCEFCGGRFPYKSSQODIQCSKCPHHS | 300 |
| Db | 241 | EAENSPPMHGCAABEEMLVPTGKCI CKAGXQCKGPTCEFCGGRFPYKSSQODIQCSKCPHHS | 300 |
| Qy | 301 | FSDEGSSSRCECEBDGYRAPSDPPYVACTRPPSAPOULIFININQTTVSLSEWSPADNDGR | 360 |
| Db | 301 | FSDEGSSSRCECEBDGYRAPSDPPYVACTRPPSAPOULIFININQTTVSLSEWSPADNDGR | 360 |
| Qy | 361 | NDVTYRILCKRCSMEQECVAPCCSNGIMPOQTGLENDYVTVMULLAHANTTPEVEAVNG | 420 |

Db 361 NDVTYRILCKRCSWEQECVPCGSNI GYMPQOTGL EDNYVTVM DLAHAANYTFEVAANG 420
Qy 421 VSDLSRQRLFAAASITTTGGAAPSOVSGVMKERYLQRSVOLSKQEPHPNGVITEYEIKY 480
Db 421 VSDLSRQRLFAAASITTTGGAAPSOVSGVMKERYLQRSVOLSKQEPHPNGVITEYEIKY 480
Qy 481 YEKQRETTYSTLTKTSTASINNLKPGTVVVFQIRAVTAAGYGNSPRLDVAATLEBASG 540
Db 481 YEKQRETTYSTLTKTSTASINNLKPGTVVVFQIRAVTAAGYGNSPRLDVAATLEBASG 540
Qy 541 KMFEATAVSSBQNVIITIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQGDDELYPH 599
Db 541 KMFEATAVSSBQNVIITIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQGDDELYPH 599

RESULT 4
JC5673
receptor tyrosine kinase (EC 2.7.-.-) Etk-ctd1 precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 20-Nov-1997 #sequence_revision 20-Nov-1997 #text_change 07-May-1999
C/Accession: JC5673
R/Author: A.H.; Muramatsu, T.; Kaneda, N.
Cell Struct. Funct. 22, 477-485, 1997
A/Title: A novel truncated variant form of Etk/MDK1 receptor tyrosine kinase is expressed
A/Reference number: JC5672; MUID:98035156; PMID:9368721
A/Accession: JC5673
A/Molecule type: mRNA
A/Residues: 1-605 <TAL>
A/Experimental source: embryo
C/Comment: This enzyme plays a regulatory role during neural development and embryogenesis
C/Keywords: brain; phosphotransferase
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-605/Product: receptor tyrosine kinase Etk-ctd1 #status predicted <MNT>
F:31-546/Domain: extracellular #status predicted <EXT>
F:31-438/Domain: fibronectin type III repeat <FNI>
F:441-534/Domain: fibronectin type III repeat <FNI>
F:549-574/Domain: transmembrane #status predicted <TM>

Query Match 94.7%; Score 3159.5; DB 2; Length 605;
Best Local Similarity 99.2%; Pred. No. 4.6e-220;
Matches 596; Conservative 0; Mismatches 0; Indels 5; Gaps 1;
Qy 1 MVQTRPSPWIIICYIMLGFHTEGAQAQKEVLLDLSKAQOTLEWISSPPSGMEISIG 60
Db 1 MVQTRPSPWIIICYIMLGFHTEGAQAQKEVLLDLSKAQOTLEWISSPPSGMEISIG 60
Qy 61 LDENYTPRTYQVQVMEPNQNNMLRTNMISKGAQRI FVELKFTLRDQNSLPVLTGTC 120
Db 61 LDENYTPRTYQVQVMEPNQNNMLRTNMISKGAQRI FVELKFTLRDQNSLPVLTGTC 120
Qy 121 ETFNLYYEEDYDGRNIRENLKYKIDTIAADESFTQGDLSGRKMKLNTVEIREIGPLSK 180
Db 121 ETFNLYYEEDYDGRNIRENLKYKIDTIAADESFTQGDLSGRKMKLNTVEIREIGPLSK 180
Qy 181 GFYLAPODVGCIALVSVKYYKKCMTIVENLAVFPDVTGSEFSSSLVEVAGTCVSSAE 240
Db 181 GFYLAPODVGCIALVSVKYYKKCMTIVENLAVFPDVTGSEFSSSLVEVAGTCVSSAE 240
Qy 241 EAENS PRMGCSAESEMLVPIGKCI CKAGYQKGDTCBPCGRFPYKSSSODLQCSRCPH 300
Db 241 EAENS PRMGCSAESEMLVPIGKCI CKAGYQKGDTCBPCGRFPYKSSSODLQCSRCPH 300
Qy 301 FSDREGSSRCCEGYYRAPSDPVPVACTRPPSAPONLIFINQTTVLSLEMSPPADNGR 360
Db 301 FSDREGSSRCCEGYYRAPSDPVPVACTRPPSAPONLIFINQTTVLSLEMSPPADNGR 360
Qy 361 NDVTYRILCKRCSWEQECVPCGSNI GYMPQOTGL EDNYVTVM DLAHAANYTFEVAANG 420
Db 361 NDVTYRILCKRCSWEQECVPCGSNI GYMPQOTGL EDNYVTVM DLAHAANYTFEVAANG 420
Qy 421 VSDLSRQRLFAAASITTTGGAAPSOVSGVMKERYLQRSVOLSKQEPHPNGVITEYEIKY 480
Db 421 VSDLSRQRLFAAASITTTGGAAPSOVSGVMKERYLQRSVOLSKQEPHPNGVITEYEIKY 480

Qy 481 YEKQRETTYSTLTKTSTASINNLKPGTVVVFQIRAVTAAGYGNSPRLDVAATLEBASG 540
Db 481 YEKQRETTYSTLTKTSTASINNLKPGTVVVFQIRAVTAAGYGNSPRLDVAATLEBASG 539
Qy 541 KMFEATAVSSBQNVIITIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQGDDELYPH 600
Db 540 ----ATAVSSBQNVIITIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQGDDELYPH 595
Qy 601 L 601
Db 596 L 596

RESULT 5
I58351
receptor protein-tyrosine kinase - human
C/Species: Homo sapiens (man)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: I58351
R/Fox, G.M.; Holte, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu, R.; Welcher, Oncogene 10, 897-905, 1995
A/Title: cDNA cloning and tissue distribution of five human Eph-like receptor protein-ty
A/Reference number: I58351; MUID:95206782; PMID:7898931
A/Accession: I58351
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-998 <RES>
A/Cross-references: UNIPROT:Q15375; GB:L36642; NID:9551607; PID:AAA74243.1; PID:9551608
C/Genetics:
A/Gene: HEK11
C/Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
F:631-897/Domain: protein kinase homology <KIN>
F:639-647/Region: protein kinase ATP-binding motif
F:920-986/Domain: SAM homology <SAM>

Query Match 94.0%; Score 3139; DB 2; Length 998;
Best Local Similarity 97.7%; Pred. No. 2.7e-218;
Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0;
Qy 1 MVQTRPSPWIIICYIMLGFHTEGAQAQKEVLLDLSKAQOTLEWISSPPSGMEISIG 60
Db 1 MVQTRPSPWIIICYIMLGFHTEGAQAQKEVLLDLSKAQOTLEWISSPPSGMEISIG 60
Qy 61 LDENYTPRTYQVQVMEPNQNNMLRTNMISKGAQRI FVELKFTLRDQNSLPVLTGTC 120
Db 61 LDENYTPRTYQVQVMEPNQNNMLRTNMISKGAQRI FVELKFTLRDQNSLPVLTGTC 120
Qy 121 ETFNLYYEEDYDGRNIRENLKYKIDTIAADESFTQGDLSGRKMKLNTVEIREIGPLSK 180
Db 121 ETFNLYYEEDYDGRNIRENLKYKIDTIAADESFTQGDLSGRKMKLNTVEIREIGPLSK 180
Qy 181 GFYLAPODVGCIALVSVKYYKKCMTIVENLAVFPDVTGSEFSSSLVEVAGTCVSSAE 240
Db 181 GFYLAPODVGCIALVSVKYYKKCMTIVENLAVFPDVTGSEFSSSLVEVAGTCVSSAE 240
Qy 241 EAENS PRMGCSAESEMLVPIGKCI CKAGYQKGDTCBPCGRFPYKSSSODLQCSRCPH 300
Db 241 EAENS PRMGCSAESEMLVPIGKCI CKAGYQKGDTCBPCGRFPYKSSSODLQCSRCPH 300
Qy 301 FSDREGSSRCCEGYYRAPSDPVPVACTRPPSAPONLIFINQTTVLSLEMSPPADNGR 360
Db 301 FSDREGSSRCCEGYYRAPSDPVPVACTRPPSAPONLIFINQTTVLSLEMSPPADNGR 360
Qy 361 NDVTYRILCKRCSWEQECVPCGSNI GYMPQOTGL EDNYVTVM DLAHAANYTFEVAANG 420
Db 361 NDVTYRILCKRCSWEQECVPCGSNI GYMPQOTGL EDNYVTVM DLAHAANYTFEVAANG 420
Qy 421 VSDLSRQRLFAAASITTTGGAAPSOVSGVMKERYLQRSVOLSKQEPHPNGVITEYEIKY 480
Db 421 VSDLSRQRLFAAASITTTGGAAPSOVSGVMKERYLQRSVOLSKQEPHPNGVITEYEIKY 480

[illegible]

| | | |
|-----------------------|------------------|---|
| QY | 582 | -----HCGSKADQEGDEE-LYFHS 600 |
| | | : : : : |
| Db | 610 | SLCAVAHPSLIWRGYSKAKQDPEEKMPFN 641 |
| | | : : : : |
| QY | 150615 | receptor-type protein-tyrosine kinase Cek7, long splice form - chicken |
| | | C:Species: Gallus gallus (chicken) |
| | | C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004 |
| | | C:Accession: I50615, I50616, I50614 |
| | | R:Siever, D.A.; Verderame, M.F. |
| | | Gene 148, 219-226, 1994 |
| QY | 150616 | A:Title: Identification of a complete Cek7 receptor protein tyrosine kinase coding sequence |
| | | A:Reference number: I50614, M01D:95047429, PMID:7958948 |
| | | A:Accession: I50615 |
| | | A:Status: translated from GB/EMBL/DBJ |
| | | A:Molecule type: mRNA |
| | | A:Residues: 1-1013 <SIB> |
| | | A:Cross-references: UNIPROT:P54755; EMBL:U03910; NID:9555617; PIDN:AAB60612.1; PID:95556 |
| | | A:Accession: I50616 |
| | | A:Status: translated from GB/EMBL/DBJ |
| | | A:Molecule type: mRNA |
| | | A:Residues: 1-572,'R',596-1013 <S12> |
| | | A:Cross-references: EMBL:U03910; NID:9555617; PIDN:AAB60613.1; PID:9555619 |
| | | A:Accession: I50614 |
| | | A:Status: translated from GB/EMBL/DBJ |
| | | A:Molecule type: mRNA |
| | | A:Residues: 1-279,'R',596-1013 <S13> |
| | | A:Cross-references: EMBL:U03910; NID:9555617; PIDN:AAB60614.1; PID:9555620 |
| | | C:Genetics: |
| | | A:Gene: Cek7 |
| | | C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h |
| | | C:Keywords: alternative splicing; ATP; transmembrane protein |
| | | F:649-915/Domain: protein kinase homology <KIN> |
| | | F:657-665/Region: protein kinase ATP-binding motif |
| | | F:938-1004/Domain: SAM homology <SAM> |
| Query Match | 53.9%; | Score 1800; DB 2; Length 1013; |
| Best Local Similarity | 55.7%; | Pred. No. 1.2e-121; |
| Matches 345; | Conservative 95; | Mismatches 135; Indels 44; Gaps 9; |
| QY | 8 | PSM--IILCYIMLGFPAHTGEAQAKEVLLDLSKAQOTLELMWISSPSGWEISGLDENY 65 |
| | | : : : : |
| Db | 15 | PCWTLGLLCAARSLILASPG-----SEVNLDBRVTWGDGLAIYPRNGWEIEGVDENY 69 |
| | | : : : : |
| QY | 66 | TPIRTYQVCQVMEPNONNMLRTNWIISKNAQRIIVEIKFTLRDNCSLPGVLGTCETENL 125 |
| | | : : : : |
| Db | 70 | APIHTYQVCQVMEQONNMLTSMWISNEGRPASSFEIKFTLRDNCSLPGGLGTCKETENM 129 |
| | | : : : : |
| QY | 126 | YYEEDVDYDGRNIRELYKIDITIADESFTQDGLGRKKIKLNEVEIGLSKKGFYLA 185 |
| | | : : : : |
| Db | 130 | YFESDDDEGRNIRENQYIKIDITIADESFTELDGLRWKLNEVEDVGLTKKGFYLA 189 |
| | | : : : : |
| QY | 186 | FQDVACIALVSVKYYKKCMTIVENLAVPDVTGSEFSILVEVGTQVS-SAEERAEEN 244 |
| | | : : : : |
| Db | 190 | FQDVACIALVSVRYVYKKCPSVIRMLARPDITITGADSSQLLEVSQVCHVHSYIDEA-- 247 |
| | | : : : : |
| QY | 245 | SPRMHCSAEGEWLVPIGKCTICAGYQOKGDTCEPCGRFPYKSSQDILQSCRCPHHSFDR 304 |
| | | : : : : |
| Db | 248 | -PKMHCSAEGEWLVPIGKCTICRAGYEKKNTQCVCRGPFKASPHSFCSCSKCPHSYILD 306 |
| | | : : : : |
| QY | 305 | EGSSHCCEGDDGYRRAPSDDPPVYACTRPPSAPKULFININQTVSLKSPSPADNGRNDVT 364 |
| | | : : : : |
| Db | 307 | EASISCLCEHYFRRESDDPTMACTRPPSAPKSAISVNETSVLEMLPPADDTGRKDV 366 |
| | | : : : : |
| QY | 365 | YRIILCRGSMWEGECVPCGSNIGYMPDQOTGLEJDNVYTVMDLLAHANTYFEVEAVNGVSDL 424 |
| | | : : : : |
| Db | 367 | YIACKKCNHSHGLCEACGSHRYRLPQOTGLKNTSVMMVVDLLAHNTYTFEIEAVNGVSDQ 426 |
| | | : : : : |
| QY | 425 | SRSQGLPAAVSLTTGQAAPSOVSGVMKERVLDQSSVQLSNQEPHPNVITFEYELKYYEKD 484 |
| | | : : : : |

Db 427 NPGARQFVSVNVTNNQAPSPVSSVKKKITKNSISLSWQEPDRPNGIILEYEIKYFEKD 466
Qy 485 QRRRTYSTLKTKSTASINNLKPGTVVYVFOIRAVTAGYGNSPRLDVATLEASGKMF 544
Db 487 Q-ETSYIIISKSTAIADGLKGSANVFOIRARTAGYGFGRFEFEI-----SP 537
Qy 545 ATAVSQNPVIIIAVAVAGTIIIVFMVFGPIIGRP-----H 562
Db 538 VLAASSDQSOIPII-VVSVTVGVILLAVIGFLISGSCDCHGCGMASLRLVAVPSLIWR 596
Qy 583 CGYSKADQEGDEE-LYFHS 600
Db 597 CGYSKAKQDPEEEKMRFHN 615

RESULT 10

A38224
protein-tyrosine kinase (EC 2.7.1.112) hek precursor - human
C/Species: Homo sapiens (man)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: A38224; B38224
R/Wicks, I.P.; Wilkenson, D.; Salvaris, E.; Boyd, A.W.
Proc. Natl. Acad. Sci. U.S.A. 89, 1611-1615, 1992
A/Title: Molecular cloning of HEK, the gene encoding a receptor tyrosine kinase expressed
A/Reference number: A38224; MUID:92179233; PMID:1311845
A/Accession: A38224
A/Molecule type: mRNA
A/Residues: 1-983 <WIC>
A/Cross-references: UNIPROT:P29320; GB:M83941; NID:g183931; PID:AAA58633.1; PID:g183932
A/Experimental source: Pre-B-cell leukemia cell line LK63
A/Note: sequence extracted from NCBI backbone (NCBI:P:86627)
A/Accession: B38224
A/Molecule type: protein
A/Residues: 21-39/810-860 <W12>
C/Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C/Keywords: ATP, autophosphorylation, glycoprotein, phosphoprotein, phosphotransferase,
F,1-20/Domain: signal sequence #status predicted <SIG>
F,21-983/Product: protein-tyrosine kinase hek #status experimental <MAT>
F,542-565/Domain: transmembrane #status predicted <TM>
F,619-685/Domain: protein kinase homology <KIN>
F,627-635/Region: protein kinase ATP-binding motif
F,232,337,391,404,493/Binding site: carboxydrate (asn) (covalent) #status predicted

Query Match 53.8%; Score 1796; DB 2; Length 983;
Best Local Similarity 57.6%; Pred. No. 2,2e-121;
Matches 329; Conservative 102; Mismatches 128; Indels 12; Gaps 5;
Qy 28 QAAKEVLLDSKAQOTLEWISSPFGMEISGLDENTYPIRTYOVQNMENPNMRLT 87
Db 25 QPSNEVNLDSKTIQGLGWIISYPSHGMESISGVDEHYTPIRTYOVQNMDSQNMRLT 84
Qy 88 NMISKGNAGIFVELKFTLRDCLNLPGLGCKETFLYYETDYGRIARENLVYKID 147
Db 85 NMPVRNAGKIVELKFTLRDCLNLPGLGCKETFLYYMESDDHGVAFREHGFKID 144
Qy 148 TIAADESFTQDGERMKKNTVEIREIGPLSKGFIYAFODVGACIALVSVKYYKKCWT 207
Db 145 TIAADESFTQMDLGRILKNTIREVGNPKKGFYLAFOVGCALVAVRVEFKCP 204
Qy 208 IVENLAIFPTTVGSESSILVEVGTGVSSAAEEAENS PMHGCABEEM VPIGKICKA 267
Db 205 TVKNLAIFPTTVP-MDSQSLVEVAGSCVNNKSKE--EDPPMYCSTEEBMLVPIGKSCNA 261
Qy 268 GYOQKGTCEPCGRFYFKSSSODLQCRPHTSPFSDGSSRCCEGEGY RASDPPIYVA 327
Db 262 GYERGMCAQCRGFGFKALDGNKKCAKCPRHSTQDGSMMCKCENNYTRADDPSPMA 321
Qy 328 CTSPSPAPNULIFININOTVSLWSPADNGGRNDVTYRILCKRCSMEQGEVCPGSGNIG 387
Db 322 CTSPSPSPRNVIISINETSVLDMWSWPLDGTGRKDVTFNIIICKKCGNNIHQCEPCSPNVR 381
Qy 388 YMPQQTLEDNYVTVMLLAHANTFEVEAVNGVSDLSRQRLPAAVSTTGQAAPEQV 447

Db 382 FLPRQGLNTVTYVTDLLAHNTYFEIDAANGVSELSPPROFAAVSTTNQAPSPVL 441
Qy 448 GVAKERVLORSVOLSWQEBEPHNGVITEYEIKYKEDERTYSTLKTSASINNLKP 507
Db 442 TTKQDTSRNSISLSWQEBEPHNGIILDYEVKYEKQEDTSTILRAGTNTISSLR 501
Qy 508 GTVYVFOIRAVTAGYGNVSPRLDVATLEASGKMFATVASEQNPVIIIAVAVAGTI 567
Db 502 DTYVFOIRARTAGYGNVSRKREFETSP-----DSFISGSSQVWMAISAVALI 554
Qy 568 IIVFMVFGPIIGRRHCGYSKADQEGDEELYE 598
Db 555 LITVVIY-VLIG-RFCGYKSKGADKRLHF 583

RESULT 11

I51549
receptor tyrosine kinase - African clawed frog
C/Species: Xenopus laevis (African clawed frog)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C/Accession: I51549
R/Wimling, R.S.; Sargent, T.D.
Mol. Cell. Biol. 13, 219-229, 1994
A/Title: Pagliaccio, a member of the Eph family of receptor tyrosine kinase genes, has 1c
A/Reference number: I51549; MUID:95001564; PMID:7918105
A/Accession: I51549
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-985 <MIN>
A/Cross-references: UNIPROT:Q91694; GB:I26099; NID:g416402; PID:AAA64464.1; PID:g416403
A/Genetics:
A/Gene: Pag
C/Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C/Keywords: ATP, transmembrane protein
F,618-684/Domain: protein kinase homology <KIN>
F,626-634/Region: protein kinase ATP-binding motif
F,907-973/Domain: SHM homology <SHM>

Query Match 53.6%; Score 1790.5; DB 2; Length 985;
Best Local Similarity 55.5%; Pred. No. 5,4e-121;
Matches 347; Conservative 98; Mismatches 161; Indels 19; Gaps 7;
Qy 11 IILCIYMLGFATG-BAQAAKEVLLDSKAQOTLEWISSP-PSGMEISGLDENTYPI 68
Db 8 ILRCGFLGCAVATGSRIVPASEVTLLDSVSGELGWIASPLGGMEEVSIIMDEKNTPI 67
Qy 69 RTYOVQNMENPNMRLTDMISGNAORIFVELKFTLRDCLNLPGLGCKETFLYYK 128
Db 68 RTYOVQNMESQNMNLRDMDIPRSGAKRYVEIKFTLRDCLNLPVMTGCKETFLYYK 127
Qy 129 ETDYDTGRNIRENLVYKIDTIAADESFTQDGERMKKNTVEIREIGPLSKGFIYAFOD 188
Db 128 ESNNDKRRFIRETOYKIDTIAADESFTQDIDRIMKNTIREVDVGPLSKGFIYAFOD 187
Qy 189 VGACIALVSVKYYKKCWTIVENLAIFPTTVGSESSILVEVGTGVSSAAEEAENS PM 248
Db 188 VGACIALVSVKYYKKCPLVRENLAQFPDITTSQDSSILVEVAGSCVNDSE--KVPK 245
Qy 249 HGSABGEMLVPIKCIKAGYQKGTCEPCGRFYFKSSSODLQCRPHTSPFSDGSS 308
Db 246 YCGADGEMLVPIKCIKAGFEHNGCCQAKGYKALSTDAKCPRHSTALRGST 305
Qy 309 RCECEGYRAPSDPEYVACTRPPSPAPNULIFININOTVSLWSPADNGGRNDVTYRIL 368
Db 306 SCICDAGYFADPDPSMPCSTRPPSPAPNULISVNETSVNLWSPNSGSRPDVSYNLV 365
Qy 369 CKRCSMEQGEVCPGSGNIGMPQQTLEDNYVTVMLLAHANTFEVEAVNGVSDLSRQ 428
Db 366 CKRCSGDLTRCSPCGSGGVHNSPOONGIKTKTKSINLQAHNTYFEVMAINVSQNP 425
Qy 429 RLFAAVSITTGQAAPEQVGVKMERVLORSVOLSWQEBEPHNGVITEYEIKYKEDOR 488
Db 426 DQAVSVITTNQAPSPVTVTOIQPKETIRHSVSLTMEPEERANGVILEYKYEKQNER 485

```
Db      484 TLIRKASTWTVTSGLKPDTTYVQPIARATARKGTSSRKKEFEFSFSP-----DSFSISS 536

Oy      551 EONPVIIIAVVAVAGTIIIVFMVFGLIGRRHCGYSKADEGDDEE-LYF 598
       | : ||| : | : | : | : | : | : | : | : | : | : | : |
Db      537 ENSGVMMIISAVALITLLTVVY-VLIG-RFCGKYKS KGTDERLHF 583

RESULT 13

receptor tyrosine kinase Mek4 - mouse
AAccession: A45583
CDate: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
CSpecies: Mus musculus (house mouse)
CAccession: A45583
CRelease: F.G.; Pasquale, E.B.; Subramani, S.
New Biol. 3, 769-778, 1991
ATitle: Identification of a new eph-related receptor tyrosine kinase gene from mouse and
AReference number: A45583; MUID:92031278; PMID:1657122
AAccession: A45583
AStatus: preliminary
AMolecule type: mRNA
AResidues: 1-963 <SAJ>
ACross-references: UNIPROT:P29319; GB:M68513; NID:G199119; PIDN:AAA9521.1; PID:G199120
ANote: sequence extracted from NCBI backbone (NCBIN:62398, NCBIF:62401)
CSuperfamily: protein-tyrosine kinase; receptor type eph; fibronectin type III repeat h
CKeywords: ATP; autophosphorylation; phosphoprotein; transmembrane protein
F:619-885/Domain: protein kinase homology <Kin>
F:627-635/Region: protein kinase ATP-binding motif

Query Match          53.4%; Score 1783.5; DB 2; Length 963;
Best Local Similarity 56.4%; Pred. No. 1,7e+120;
Matches 334; Conservative 104; Mismatches 135; Indels 19; Gaps 8;
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| Query Match | 53.4% | Score 1783.5 | DB 2 | Length 983 |
|-----------------------|---|--------------------|-----------|------------|
| Best Local Similarity | 56.4% | Pred. No. 1.7e-120 | | |
| Match 334 | Conservative 104 | Mismatches 135 | Indels 19 | Gaps 8 |
| Db | 13 LCYIMLGG--FAHTGE--AQAAKEVLLDLSKAQOOTELEWISSPPSGMEBISGLDENYTP | 67 | | |
| Qy | 13 LCYIMLGG--FAHTGE--AQAAKEVLLDLSKAQOOTELEWISSPPSGMEBISGLDENYTP | 67 | | |
| Db | 5 LSLIVLLGCCVSLSCSELSPQSPSENVVLLDLSKTIQGLGLWISYPSHGWBEISGVDEHYTP | 64 | | |
| Qy | 5 LSLIVLLGCCVSLSCSELSPQSPSENVVLLDLSKTIQGLGLWISYPSHGWBEISGVDEHYTP | 64 | | |
| Db | 68 IRTTYQVCQWMPRONNWLRTNWLISKNAQRIPEBLKLTPLDNCNLSPLGLCTKTFENLYY | 127 | | |
| Qy | 68 IRTTYQVCQWMPRONNWLRTNWLISKNAQRIPEBLKLTPLDNCNLSPLGLCTKTFENLYY | 127 | | |
| Db | 65 IRTTYQVCNMDHSQNNWLRTNWLWPNRSQKRIYELKFTLRQNSIPLVLGCTKTFENLYY | 124 | | |
| Qy | 65 IRTTYQVCNMDHSQNNWLRTNWLWPNRSQKRIYELKFTLRQNSIPLVLGCTKTFENLYY | 124 | | |
| Db | 128 YETDVTGTNRINENLVYKIDITLADESFTQDGLGERGKMTNTEVREISPLSKGFIYAFQ | 187 | | |
| Qy | 128 YETDVTGTNRINENLVYKIDITLADESFTQDGLGERGKMTNTEVREISPLSKGFIYAFQ | 187 | | |
| Db | 125 MSDSD-DHGKRFEPHQETKIDITLADESFTQMDLGRILKLTNTEIREVQPVAKKGFIYAFQ | 183 | | |
| Qy | 125 MSDSD-DHGKRFEPHQETKIDITLADESFTQMDLGRILKLTNTEIREVQPVAKKGFIYAFQ | 183 | | |
| Db | 188 DVGACIALVSVKYKYKCMFTVENLAVFPDVTGSEFSSLYEVRQTCVSSAEEEAENSPPR | 247 | | |
| Qy | 188 DVGACIALVSVKYKYKCMFTVENLAVFPDVTGSEFSSLYEVRQTCVSSAEEEAENSPPR | 247 | | |
| Db | 184 DVGACIALVSVRYYFKKCPFTVKNLAMPDTPV-MDSQSLVEVRGSCVNNKSKE--EDBP | 240 | | |
| Qy | 184 DVGACIALVSVRYYFKKCPFTVKNLAMPDTPV-MDSQSLVEVRGSCVNNKSKE--EDBP | 240 | | |
| Db | 248 MHCSAGEMLVPIGKICICAKGYOQKDTCEPCGRRFFKSSSQDLCSCSPHSPFDRGCS | 307 | | |
| Qy | 248 MHCSAGEMLVPIGKICICAKGYOQKDTCEPCGRRFFKSSSQDLCSCSPHSPFDRGCS | 307 | | |
| Db | 241 MNCSTEGEMLVPIGKICTNAGYEREGFTCOACRGRFFKASGAAKCAACPHSSSTQDEGCS | 300 | | |
| Qy | 241 MNCSTEGEMLVPIGKICTNAGYEREGFTCOACRGRFFKASGAAKCAACPHSSSTQDEGCS | 300 | | |
| Db | 308 SRCECEDGYRASPDPVYACTRPPSAPOMLFININQTVSLSEASPANDGGRNDVYRI | 367 | | |
| Qy | 308 SRCECEDGYRASPDPVYACTRPPSAPOMLFININQTVSLSEASPANDGGRNDVYRI | 367 | | |
| Db | 301 MNCRCENNYFRAEKDPPMACARPPSAPRVININQTVSLDMSWPLDGTGRKQDITNI | 360 | | |
| Qy | 301 MNCRCENNYFRAEKDPPMACARPPSAPRVININQTVSLDMSWPLDGTGRKQDITNI | 360 | | |
| Db | 368 LCKRCGMEQECVPCGSSNIGYMPQQTGLENDNYTMDLLAHANTTFEVEAYNVGUSDLSRS | 427 | | |
| Qy | 368 LCKRCGMEQECVPCGSSNIGYMPQQTGLENDNYTMDLLAHANTTFEVEAYNVGUSDLSRS | 427 | | |
| Db | 361 ICKKCGMNRROCEPCSPNHFILPROGLTNTVTVLTLAHNTYTFELDANVGSSELSP | 420 | | |
| Qy | 361 ICKKCGMNRROCEPCSPNHFILPROGLTNTVTVLTLAHNTYTFELDANVGSSELSP | 420 | | |
| Db | 428 ORLPAVASTTGGQAASQVSGVWKERVLRQSVOLSMOEPHPNVCITYTEIKYKQDRE | 487 | | |
| Qy | 428 ORLPAVASTTGGQAASQVSGVWKERVLRQSVOLSMOEPHPNVCITYTEIKYKQDRE | 487 | | |
| Db | 421 PRQYAAVASTTMDAASPVTITKKDRISRSISLSWQEPHPNGIILDYEVKTYQKQDE | 480 | | |
| Qy | 421 PRQYAAVASTTMDAASPVTITKKDRISRSISLSWQEPHPNGIILDYEVKTYQKQDE | 480 | | |
| Db | 488 RTYSTLKTSSTASINNLKPGIYVFOIRAQVTAAGYNGYSPRLDVAATLEASGKMFQATA | 547 | | |
| Qy | 488 RTYSTLKTSSTASINNLKPGIYVFOIRAQVTAAGYNGYSPRLDVAATLEASGKMFQATA | 547 | | |
| Db | 481 TSYTILRARGTNTTISLKPDTTYVFOIRARTAGYGTNSKRFEPETSP-----DSFS | 533 | | |
| Qy | 481 TSYTILRARGTNTTISLKPDTTYVFOIRARTAGYGTNSKRFEPETSP-----DSFS | 533 | | |
| Db | 548 VSSQNPVYIIIVAVNAGTIIIVFMVFGFIIGRRHCGYSKADQDGDDE-LVF | 598 | | |
| Qy | 548 VSSQNPVYIIIVAVNAGTIIIVFMVFGFIIGRRHCGYSKADQDGDDE-LVF | 598 | | |
| Db | 534 IGSNSHVVMIAISAAVAITILT-VVTYVLVGRFGCGYHKSISAAEERLHP | 583 | | |
| Qy | 534 IGSNSHVVMIAISAAVAITILT-VVTYVLVGRFGCGYHKSISAAEERLHP | 583 | | |

RESULT 14
178844
receptor protein-tyrosine kinase - human
C/Species: Homo sapiens (man)
C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 03-Jul-2004
C/Accession: I78844
R/Ref: G.M.; Holte, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu, R.; Welcher, Oncogene 10, 897-905, 1995
A/Title: cDNA cloning and tissue distribution of five human EPH-like receptor protein-ty
A/Reference number: 158351; MUID:95206782; PMID:7898931
A/Accession: I78844
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-986 <RSS>
A/Cross-references: UNIPROT:P54764; GB:I36645; NID:G551613; PIDN:AAA74246.1; PID:G551614
C/Genetics:
A/Gene: HEK8
C/Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
F:619-685/Domain: protein kinase homology <KIN>
F:908-974/Domain: SAM homology <SAM>

Query Match 52.2%; Score 1741.5; DB 2; Length 966;
Best Local Similarity 54.0%; Pred. No. 1.9e-117; Mismatches 149; Indels 19; Gaps 7;
Matches 327; Conservative 111; Mismatches 149; Indels 19; Gaps 7;
QY 30 AKEVLLDSKAQOQTELEWISSP-PSGWEIISGLDENTYPIRTYQVCQWMEINQNNMLRTN 88
DB 28 ANEVTLTDSRSVQGLGMIASPLEGMEVSIIMDEKOTPIRTYQVCNMEHQNNMLRTD 87
QY 89 WISGMGNQRIFFVELKFTLRDQNSLPGLGCTCKETFNYYETDPTGRNTHENLYYKIDT 148
DB 88 WITREGQRYVIEIKFTLRDQNSLPGLGCTCKETFNYYETDPTGRNTHENLYYKIDT 147
QY 149 IAADESTFQDGLGERKKMLNTEVEIEIGLSKGFYLAFOVGAACIALVSVYKKKWTI 208
DB 148 IAADESTFQDGLGERKKMLNTEVEIEIGLSKGFYLAFOVGAACIALVSVYKKKWTI 207
QY 209 VENIAVPDTVTGSEFSSSLVEVGTGVSAAEEAENSPRMHCASAEGLVYIGKCIKAG 268
DB 208 VKNIAQPPDTITGADTSLVEVRGS CVNNSE--KDVPMKMGADGEMLVYIGKCIKAG 265
QY 269 YQKQGDTCPCGRFRFYSSSODLQCSRCPHSPFSDREGSSRCEDGYVRAASPPRYAC 328
DB 266 HEERSGECQACKIGYVALSTDAATCAKCPHSPVSWEGATSCDTRGPRADNDASMP 325
QY 329 TRPSAPQNLIFINQTTVSLSESPPADNGRNDVYRIILCKRC-SWEOG3CVVPCGSNIG 387
DB 326 TRPSAPNLINISNNETSVLEMSFPQNTGRODISYNNVCKKCGADDPKCRPCSGVH 385
QY 388 YMQQGTLENDYVTMDLAAHNTFEVEAVNGVDSLRSQRLFAAVSITTGQAAPSOVS 447
DB 386 YTPQONGLKTTKVYSITDILAHNTYTFEIMAVNGVSKNPNPDQSVSTVITNQAPSSIA 445
QY 448 GWKMERVLQSVQSWQEPHNGVITEYIKYKQKORERTYTLTKTSASINLKP 507
DB 446 LVQAKETRYRSVALAMLEPRPNVILEYKYEKKQNEKSYKIVTAAANDIKLNP 505
QY 508 GTTVVFOIRAVTAAGYNSPRLDVATLEASGKMFATAVSSQONVILIAVAAGTI 567
DB 506 LITSVFHVARATAGYGDPSLEPVT--NTVESRIIGDANSTVLL--SVSGSV 557
QY 568 IL-VFMVFGTIGRHGCKSKADQGDDELYFHSLYBERGDMEKTOHN-----KMTI 620
DB 558 VLVVILIAFAFVISRBRKSKAKQADBEKHLNGVRYVDPFTYEDPNQAVREFAKEID 617
QY 621 ASCSRL 626
DB 618 ASCIKI 623

RESULT 15
S78059
protein-tyrosine kinase (EC 2.7.1.112) Eph precursor - mouse

C/Species: Mus musculus (house mouse)
C/Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C/Accession: S78059; S30505; I58366
R/Charney, P.
submitted to the EMBL Data Library, March 1992
A/Reference number: S78059
A/Accession: S78059
A/Molecule type: mRNA
A/Residues: 1-986 <CHA>
A/Cross-references: UNIPROT:Q00137; EMBL:X65138; NID:G54083; PIDN:CAA6268.1; PID:G54084
R/Gillard-Hebenstreit, P.; Nieto, M.A.; Frain, M.; Mattei, M.G.; Chastier, A.; Wilkinson, Oncogene 7, 2499-2506, 1992
A/Title: An Eph-related receptor protein tyrosine kinase gene segmentally expressed in ct
A/Reference number: S30496; MUID:93096484; PMID:1281307
A/Accession: S30505
A/Molecule type: mRNA
A/Residues: 1-31,55-986 <GIL>
A/Cross-references: EMBL:X65138
C/Genetics:
A/Gene: Sek
C/Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C/Keywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferase; t
F:1-15/Domain: signal sequence #status predicted <SIG>
F:1-15/Domain: signal sequence #status predicted <SIG>
F:1-986/Product: protein-tyrosine kinase Eph #status predicted <MAT>
F:548-569/Domain: transmembrane #status predicted <TM>
F:619-685/Domain: protein kinase homology <KIN>
F:627-635/Region: protein kinase ATP-binding motif
F:908-974/Domain: SAM homology <SAM>
F:235,340,408,423/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 51.6%; Score 1723; DB 2; Length 966;
Best Local Similarity 52.3%; Pred. No. 4e-116; Mismatches 162; Indels 20; Gaps 8;
Matches 328; Conservative 117; Mismatches 162; Indels 20; Gaps 8;
QY 10 WITLCYIWLGFPAHTG-EAQAKVLLDSKAQOQTELEWISSP-PSGWEIISGLDENTYPI 67
DB 7 FILSPFLGCDVATSRVYPAHEVTLDSRSVQGLGMIASPLEGMEVSIIMDEKOTPI 66
QY 68 IRTYQVCQWMEINQNNMLRTNWSKNAQRIFFVELKFTLRDQNSLPGLGCTCKETFNLY 127
DB 67 IRTYQVCNMEHQNNMLRTDITREGAQRYVIEIKFTLRDQNSLPGLGCTCKETFNLY 126
QY 128 YETDPTGRNTHENLYYKIDTIAADESTFQDGLGERKKMLNTEVEIEIGLSKGFYLAFO 167
DB 127 YESDNDKERIRFESQCKTDTIAADESTFQVDIGDIMKMLNTEIRVGLSKGFYLAFO 166
QY 188 DVAGACIALVSVYKKKWTIYENIAVPDTVTGSEFSSSLVEVGTGVSAAEEAENSPR 247
DB 187 DVAGACIALVSVYKKKWTIYENIAVPDTVTGSEFSSSLVEVGTGVSAAEEAENSPR 244
QY 248 MHCSAGEMLVPIGKICVKAQYQKGDTCPCGRFRFYSSSODLQCSRCPHSPFSDREGS 307
DB 245 MYCGADGEMLVPIGKICVKAQYQKGDTCPCGRFRFYSSSODLQCSRCPHSPFSDREGS 304
QY 308 SRECEGDYVRAASDPYVACTRPSAPQNLIFINQTTVSLSESPPADNGRNDVYRIIL 367
DB 305 TSCCTCRGFPRAANDASMECTRPSPAPNLINISNNETSVLEMSFPQNTGRODISY 364
QY 368 LCKRC-SWEOG3CVVPCGSNIGYMQQGTLENDYVTMDLAAHNTFEVEAVNGVDSLRS 426
DB 365 VCKKCGADPSKCRPCGSGVHTYTPQONGLKTRTVSITDILAHNTYTFEIMAVNGVSK 424
QY 427 SQRLFAVSLITGQAAPSOVSQWMEKRYLQSVQSWQEPHNGVITEYIKYKQKORERTY 486
DB 425 SPDQSVSTVITNQAPSSIALVQAKETRYRSVALAMLEPRPNVILEYKYEKKQNEK 484
QY 487 ERTYSLTKTSISASINLKGTVYVFOIRAVTAAGYNSPRLDVATLEASGKMFATAV 546
DB 485 ERSYRIVRTAARTDIKGLNPILTSYFVHVARATAGYGDPSLEPVT-----NTVPSR 538
QY 547 AVSSEQNPVILIAVAAGTIIL-VFMVFGTIGRHGCKSKADQGDDELYFHSLYRER 605
DB 539 ITDGDANSTVLL--SVSGSVLVVILIAFAFVISRBRKSKAKQADBEKHLNGVRY 596

Qy 606 GDGMEKTOHKK-----KMMIASCRL 626
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Db 597 VDPFTYEDDPNQAVRFAKEIDASCIXI 623
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Search completed: August 23, 2005, 08:33:12
Job time : 18.7136 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 23, 2005, 08:30:14 ; Search time 112.437 Seconds
(without alignments)
2180.182 Million cell updates/sec

Title: US-10-073-064-5

Perfect score: 3338

Sequence: 1 MVVQTRPSPWILLCYWLLG.....DGMEXTQHNKKMTJASCSRL 626

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

1759131

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|---------------------|
| 1 | 3191 | 95.6 | 998 | 10 | US-09-823-187-42 |
| 2 | 3175 | 95.1 | 998 | 10 | US-09-823-187-43 |
| 3 | 3139 | 94.0 | 945 | 15 | US-10-112-944-260 |
| 4 | 3139 | 94.0 | 998 | 10 | US-09-823-187-40 |
| 5 | 3031.5 | 90.8 | 993 | 10 | US-09-823-187-39 |
| 6 | 3031.5 | 90.8 | 993 | 10 | US-09-823-187-41 |
| 7 | 1841 | 55.2 | 991 | 10 | US-09-823-187-44 |
| 8 | 1836.5 | 55.0 | 1041 | 18 | US-10-840-512-215 |
| 9 | 1830.5 | 54.8 | 953 | 14 | US-10-412-277-7 |
| 10 | 1827 | 54.7 | 991 | 17 | US-10-733-923-13667 |
| 11 | 1819 | 54.5 | 1005 | 15 | US-10-029-020-63 |

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| 12 | 1817 | 54.4 | 1037 | 14 | US-10-316-124-3 | Sequence 3, Appli |
| 13 | 1817 | 54.4 | 1037 | 15 | US-10-353-690-40 | Sequence 40, Appli |
| 14 | 1817 | 54.4 | 1037 | 20 | US-11-064-551-3 | Sequence 3, Appli |
| 15 | 1806.5 | 54.1 | 975 | 14 | US-10-412-277-8 | Sequence 8, Appli |
| 16 | 1800 | 53.9 | 1013 | 17 | US-10-732-923-13668 | Sequence 13668, A |
| 17 | 1796 | 53.8 | 666 | 9 | US-09-771-161A-136 | Sequence 136, App |
| 18 | 1796 | 53.8 | 983 | 9 | US-09-771-161A-227 | Sequence 227, App |
| 19 | 1796 | 53.8 | 983 | 14 | US-10-205-823-97 | Sequence 97, Appli |
| 20 | 1796 | 53.8 | 983 | 14 | US-10-345-680-2 | Sequence 2, Appli |
| 21 | 1796 | 53.8 | 983 | 15 | US-10-295-027-602 | Sequence 602, App |
| 22 | 1796 | 53.8 | 983 | 15 | US-10-029-020-59 | Sequence 59, Appli |
| 23 | 1796 | 53.8 | 983 | 17 | US-10-794-514A-467 | Sequence 467, App |
| 24 | 1796 | 53.8 | 983 | 18 | US-10-489-125B-11 | Sequence 11, Appli |
| 25 | 1790.5 | 53.6 | 985 | 15 | US-10-029-020-61 | Sequence 61, Appli |
| 26 | 1783.5 | 53.4 | 968 | 14 | US-10-412-277-6 | Sequence 6, Appli |
| 27 | 1783.5 | 53.4 | 923 | 17 | US-10-732-923-13675 | Sequence 13675, A |
| 28 | 1741.5 | 52.2 | 921 | 9 | US-09-805-020-52 | Sequence 52, Appli |
| 29 | 1741.5 | 52.2 | 986 | 16 | US-10-723-860-597 | Sequence 597, App |
| 30 | 1734.5 | 52.0 | 1104 | 9 | US-09-982-610-36 | Sequence 36, Appli |
| 31 | 1701.5 | 51.0 | 935 | 15 | US-10-449-569-36 | Sequence 36, Appli |
| 32 | 1701.5 | 51.0 | 992 | 10 | US-09-973-424A-5 | Sequence 5, Appli |
| 33 | 1701.5 | 51.0 | 992 | 10 | US-09-973-424A-53 | Sequence 53, Appli |
| 34 | 1701.5 | 51.0 | 992 | 17 | US-10-691-165-5 | Sequence 5, Appli |
| 35 | 1701.5 | 51.0 | 1005 | 15 | US-10-449-569-2 | Sequence 53, Appli |
| 36 | 1701.5 | 51.0 | 1005 | 15 | US-10-449-569-2 | Sequence 3, Appli |
| 37 | 1701.5 | 51.0 | 1012 | 15 | US-10-168-582-3 | Sequence 34, Appli |
| 38 | 1699.5 | 50.9 | 928 | 15 | US-10-449-569-14 | Sequence 52, Appli |
| 39 | 1695 | 50.8 | 991 | 17 | US-09-973-424A-52 | Sequence 52, Appli |
| 40 | 1695 | 50.8 | 991 | 17 | US-10-691-165-52 | Sequence 52, Appli |
| 41 | 1671 | 50.1 | 1035 | 15 | US-10-029-020-50 | Sequence 20, Appli |
| 42 | 1665.5 | 49.9 | 1036 | 10 | US-09-971-708-2 | Sequence 2, Appli |
| 43 | 1665.5 | 49.9 | 1036 | 14 | US-10-245-752-104 | Sequence 104, App |
| 44 | 1665.5 | 49.9 | 1036 | 14 | US-10-245-859-104 | Sequence 104, App |
| 45 | 1665.5 | 49.9 | 1036 | 14 | US-10-245-103-104 | Sequence 104, App |

ALIGNMENTS

RESULT 1
US-09-823-187-42
; Sequence 42, Application US/09823187
; Publication No. US20030096952A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine
; APPLICANT: Gubey, Vladimir Y
; APPLICANT: Liu, Xiaohong
; APPLICANT: Majumder, Kumar
; APPLICANT: Padigaru, Muralidhar
; APPLICANT: Patirajan, Meera
; APPLICANT: Shinkets, Richard A
; APPLICANT: Spaderina, Steven K
; APPLICANT: Spytek, Kimberly J
; APPLICANT: Taupier, Raymond J
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-745
; CURRENT APPLICATION NUMBER: US/09/823,187
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/193,339
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/193,205
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/195,343
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/195,088
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,005
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,792
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: 60/196,556
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: 60/197,081

;; PRIOR FILING DATE: 2000-04-13
;; PRIOR APPLICATION NUMBER: 60/197,525
;; PRIOR FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/197,087
;; PRIOR FILING DATE: 2000-04-14
;; NUMBER OF SEQ ID NOS: 103
;; SOFTWARE: Patentln Ver. 2.1
;; SEQ ID NO 42
;; LENGTH: 998
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-09-823-187-42

Query Match 95.6%; Score 3191; DB 10; Length 998;
Best Local Similarity 100.0%; Pred. No. 1,1e-243;
Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MVOGTRPSPWIIICYYIMLGFPAHTGEAQAQAEVLLDSKAQQTLEWISSPPSGWEIISG 60
QY 61 LDENVTPRTYOVQVQVMEPNQNNMLRTNWSKGAQRI FVELKFTLADCNLSLPGVLTGTC 120
DB 61 LDENVTPRTYOVQVQVMEPNQNNMLRTNWSKGAQRI FVELKFTLADCNLSLPGVLTGTC 120
QY 121 ETFNLYYETDYDGRNIRENLVYKIDTIADESFTQDGERKMKLNTYVREIIGPLSKK 180
DB 121 ETFNLYYETDYDGRNIRENLVYKIDTIADESFTQDGERKMKLNTYVREIIGPLSKK 180
QY 181 GFYLAFOVQACIALVSVKYYKKCWITVENLAVFPDVTGSEFSSLVE/RGTCVSSAAE 240
DB 181 GFYLAFOVQACIALVSVKYYKKCWITVENLAVFPDVTGSEFSSLVE/RGTCVSSAAE 240
QY 241 EAENSPRMHGSAEGEWLVPVIGKCI CKAGYQOKGDTCEPCGRFPYKSSODLQCSRCPHIS 300
DB 241 EAENSPRMHGSAEGEWLVPVIGKCI CKAGYQOKGDTCEPCGRFPYKSSODLQCSRCPHIS 300
QY 301 FSDREGSSRCCEGCEGYRAPSDPPYVACTRPPSAQNLIFININQTTVSL3MSPPADNGR 360
DB 301 FSDREGSSRCCEGCEGYRAPSDPPYVACTRPPSAQNLIFININQTTVSL3MSPPADNGR 360
QY 361 NDVTYRILCKRCSEWQEGCEVPCGSNIGYMPQQTGLEDDNYVTVMDLAHANTFEEVAVNG 420
DB 361 NDVTYRILCKRCSEWQEGCEVPCGSNIGYMPQQTGLEDDNYVTVMDLAHANTFEEVAVNG 420
QY 421 VSDLSRQRLFAAVSITTTGAAPQVSGVMKERVLQRSVOLSWQEPHPNGVITEYEIKY 480
DB 421 VSDLSRQRLFAAVSITTTGAAPQVSGVMKERVLQRSVOLSWQEPHPNGVITEYEIKY 480
QY 481 YEKQRERTYSTLTKTSASINNLKPGTYVVFQIRAVTAAGYGNYSBRLDVATLEASG 540
DB 481 YEKQRERTYSTLTKTSASINNLKPGTYVVFQIRAVTAAGYGNYSBRLDVATLEASG 540
QY 541 KMFEATAVSSQNPVILIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQGDDELYFH 599
DB 541 KMFEATAVSSQNPVILIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQGDDELYFH 599

RESULT 2

US-09-823-187-43
;; Sequence 43, Application US/09823187
;; Publication No. US20030096952A1
;; GENERAL INFORMATION:
;; APPLICANT: Burgess, Catherine
;; APPLICANT: Gusev, Vladimir Y
;; APPLICANT: Liu, Xiaohong
;; APPLICANT: Majumder, Murud
;; APPLICANT: Padigaru, Muralidhar
;; APPLICANT: Patcurajan, Meera
;; APPLICANT: Shimketa, Richard A
;; APPLICANT: Spaderna, Steven K
;; APPLICANT: Spytek, Kimberly
;; APPLICANT: Taupier, Raymond J

;; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;; FILE REFERENCE: 15966-745
;; CURRENT APPLICATION NUMBER: US/09/823,187
;; CURRENT FILING DATE: 2001-03-29
;; PRIOR APPLICATION NUMBER: 60/193,339
;; PRIOR FILING DATE: 2000-03-30
;; PRIOR APPLICATION NUMBER: 60/193,205
;; PRIOR FILING DATE: 2000-03-30
;; PRIOR APPLICATION NUMBER: 60/195,343
;; PRIOR FILING DATE: 2000-04-05
;; PRIOR APPLICATION NUMBER: 60/195,088
;; PRIOR FILING DATE: 2000-04-06
;; PRIOR APPLICATION NUMBER: 60/195,005
;; PRIOR FILING DATE: 2000-04-06
;; PRIOR APPLICATION NUMBER: 60/195,792
;; PRIOR FILING DATE: 2000-04-10
;; PRIOR APPLICATION NUMBER: 60/196,556
;; PRIOR FILING DATE: 2000-04-11
;; PRIOR APPLICATION NUMBER: 60/197,081
;; PRIOR FILING DATE: 2000-04-13
;; PRIOR APPLICATION NUMBER: 60/197,525
;; PRIOR FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/197,087
;; NUMBER OF SEQ ID NOS: 103
;; SOFTWARE: Patentln Ver. 2.1
;; SEQ ID NO 43
;; LENGTH: 998
;; TYPE: PRT
;; ORGANISM: Rattus norvegicus
US-09-823-187-43

Query Match 95.1%; Score 3175; DB 10; Length 998;
Best Local Similarity 99.2%; Pred. No. 2e-242;
Matches 594; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MVOGTRPSPWIIICYYIMLGFPAHTGEAQAQAEVLLDSKAQQTLEWISSPPSGWEIISG 60
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DB 61 LDENVTPRTYOVQVQVMEPNQNNMLRTNWSKGAQRI FVELKFTLADCNLSLPGVLTGTC 120
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DB 121 ETFNLYYETDYDGRNIRENLVYKIDTIADESFTQDGERKMKLNTYVREIIGPLSKK 180
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DB 181 GFYLAFOVQACIALVSVKYYKKCWITVENLAVFPDVTGSEFSSLVEVRGTCVSSAAE 240
QY 241 EAENSPRMHGSAEGEWLVPVIGKCI CKAGYQOKGDTCEPCGRFPYKSSODLQCSRCPHIS 300
DB 241 EAENSPRMHGSAEGEWLVPVIGKCI CKAGYQOKGDTCEPCGRFPYKSSODLQCSRCPHIS 300
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DB 301 FSDREGSSRCCEGCEGYRAPSDPPYVACTRPPSAQNLIFININQTTVSL3MSPPADNGR 360
QY 361 NDVTYRILCKRCSEWQEGCEVPCGSNIGYMPQQTGLEDDNYVTVMDLAHANTFEEVAVNG 420
DB 361 NDVTYRILCKRCSEWQEGCEVPCGSNIGYMPQQTGLEDDNYVTVMDLAHANTFEEVAVNG 420
QY 421 VSDLSRQRLFAAVSITTTGAAPQVSGVMKERVLQRSVOLSWQEPHPNGVITEYEIKY 480
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QY 481 YEKQRERTYSTLTKTSASINNLKPGTYVVFQIRAVTAAGYGNYSBRLDVATLEASG 540
DB 481 YEKQRERTYSTLTKTSASINNLKPGTYVVFQIRAVTAAGYGNYSBRLDVATLEASG 540
QY 541 KMFEATAVSSQNPVILIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQGDDELYFH 599

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|----|-----|---|-----|
| Qy | 1 | MMVQTPEPMIIICYIMLGFPAHTGAQAQAKVLLIDSKAQOTLEMIWISSPSSMEISG | 60 |
| Db | 1 | MFQRTPEPMIIICYIMLRFPAHTGAQAQAKVLLIDSKAQOTLEMIWISSPSSMEISG | 60 |
| Qy | 61 | LDENYTPIRTYQVCQMEPNONNMILRTWISKGNQRI FVELKFLTRDQNSLPVGLTCK | 120 |
| Db | 61 | LDENYTPIRTYQVCQMEPNONNMILRTWISKGNQRI FVELKFLTRDQNSLPVGLTCK | 120 |
| Qy | 121 | ETENLVYYEEDYDTGNIRENLYVKIDTIAADESFQODLGBRKMKLNTVEIREIGPLSK | 180 |
| Db | 121 | ETENLVYYEEDYDTGNIRENLYVKIDTIAADESFQODLGBRKMKLNTVEIREIGPLSK | 180 |
| Qy | 181 | GFYLAFOQVACIALVSVKRYKKCKWTIVENLAVFPDVTGSSPSSLVEVKGTCVSSAEE | 240 |
| Db | 181 | GFYLAFOQVACIALVSVKRYKKCKWSIIENLAIFPDVTGSSPSSLVEVKGTCVSSAEE | 240 |
| Qy | 241 | EAENSPRMHCSAGEWLVPIGKICICAKGYQOQGDPCFCGRFRYSSSGODLQCSRCPTHS | 300 |
| Db | 241 | EAENAPRMHCSAGEWLVPIGKICICAKGYQOQGDPCFCGRGFYSSSGODLQCSRCPTHS | 300 |

| | | | |
|----|-----|---|-----|
| Qy | 301 | FSRSESSSCEDEDDGYRASPDPVYACTRPSPSAQNLFININTVYLSLESPADNGR | 360 |
| Db | 301 | FSDESSSSCEDEDDGYRASPDPVYACTRPSPSAQNLFININTVYLSLESPADNGR | 360 |
| Qy | 361 | NDVYTHLLCKRSMWEGECVPCGSGNIGYMPQDTGLEDDYVTVMOLLAAHATTFEVAANG | 422 |
| Db | 361 | NDVYTHLLCKRSMWEGECVPCGSGNIGYMPQDTGLEDDYVTVMOLLAAHATTFEVAANG | 420 |
| Qy | 421 | VSDLSRSQRLFAVAISITTGQAAPSVSGVMKERVLDQRSVOLSWQEPHNPVITREYIKY | 480 |
| Db | 421 | VSDLSRSQRLFAVAISITTGQAAPSVSGVMKERVLDQRSVELSWQEPHNPVITREYIKY | 480 |
| Qy | 481 | YEDQSEERTYSLTKTSSASINNLKPGTVYVFOGRANTAAAGYGNYSRDLVALTEASG | 540 |
| Db | 481 | YEDQSEERTYSLTKTSSASINNLKPGTVYVFOGRATTAAGYGNYSRDLVALTEATG | 540 |
| Qy | 541 | KMEFATAVSSEQNPVILIIVAVAGTITLIVFVFGFIIIGRAHCGYSKADQGEDELYFH | 599 |
| Db | 541 | KMEFATAVSSEQNPVILIIVAVAGTITLIVFVFGFIIIGRAHCGYSKADQGEDELYFH | 599 |

RESULT 4
US-09-823-187-40

Sequence 40, Application US/098
Publication No. US20030096952A1
GENERAL INFORMATION:

? APPLICANT: Burgess, Catherine
 ? APPLICANT: Gusev, Vladimir Y
 ? APPLICANT: Liu, Xiaohong
 ? APPLICANT: Majumder, Kumud
 ? APPLICANT: Padigar, Muralidhar
 ? APPLICANT: Patturajan, Meera
 ? APPLICANT: Shinkets, Richard A
 ? APPLICANT: Spaderna, Steven K
 ? APPLICANT: Spytek, Kimberly
 ? APPLICANT: Tupper, Raymond J
 ? TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME

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FILE REFERENCE: 15966-745
CURRENT APPLICATION NUMBER: US/09/823,187
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/193,339
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/193,205
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/195,343
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: 60/195,088
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,005
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,792
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: 60/196,556
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: 60/197,081
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 60/197,525
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/197,087
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 103
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 40
LENGTH: 998
TYPE: PRT
ORGANISM: Homo sapiens
US-09-823-187-40

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|-----------------------|------------------|---------------------|-----------|-------------|
| Query Match | 94.0%; | Score 3139; | DB 10; | Length 998; |
| Best Local Similarity | 97.7%; | Pred. No. 1.4e-239; | | |
| Matches 585; | Conservative 10; | Mismatches 4; | Indels 0; | Gaps 0 |

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Qy 1 MVOTRFPSPWIIICLYMLGFPAHTGEAQAKEVILLDSKAQOTELEWISSPPSGMEETISG 60
Db 1 MVOTRFPSPWIIICLYMLGFPAHTGEAQAKEVILLDSKAQOTELEWISSPPSGMEETISG 60
Qy 61 LDENVTPRTYOVQVQWNEPNNMRLTNWISKNAQRIFVELKFTLRDCLSPGLGTCK 120
Db 61 LDENVTPRTYOVQVQWNEPNNMRLTNWISKNAQRIFVELKFTLRDCLSPGLGTCK 120
Qy 121 ETFNLYYEETDYGGRNIRENLYVKIDITIADESFQDGLGERKMKLNTREIGPLSKK 180
Db 121 ETFNLYYEETDYGGRNIRENLYVKIDITIADESFQDGLGERKMKLNTREIGPLSKK 180
Qy 181 GFYLAPODVGACIALVSVKYYKKCWITVENLAVPDTVTGSEFSSLVEVRGTVCSSAEE 240
Db 181 GFYLAPODVGACIALVSVKYYKKCWITVENLAVPDTVTGSEFSSLVEVRGTVCSSAEE 240
Qy 241 EAENSPRMHCSAEGEWLVPIGKCIKAGYQOKGDTCEPCGRRFYKSSQDLQSCRCPHIS 300
Db 241 EAENSPRMHCSAEGEWLVPIGKCIKAGYQOKGDTCEPCGRRFYKSSQDLQSCRCPHIS 300
Qy 301 FSDREGSSRCCEDEGYRAPSDPPYVACTRPPSAQNLIENINOTTVSLFWSPPADNGCR 360
Db 301 FSDREGSSRCCEDEGYRAPSDPPYVACTRPPSAQNLIENINOTTVSLFWSPPADNGCR 360
Qy 361 NDVTYRILCKRCSEWQECVPCGSNIGMPQOTGLEDNVYTVMDLAAHAYTFEVEAVNG 420
Db 361 NDVTYRILCKRCSEWQECVPCGSNIGMPQOTGLEDNVYTVMDLAAHAYTFEVEAVNG 420
Qy 421 VSDLSRQRLFAAASITTGGAAPSOVSGWKEKRVLQRSVQELSWQEPHPNGVITEYEIKY 480
Db 421 VSDLSRQRLFAAASITTGGAAPSOVSGWKEKRVLQRSVQELSWQEPHPNGVITEYEIKY 480
Qy 481 YEKQRETTYSTLTKTSTASINNLKPGTVVFOIRAVTAAGYGNYSPLDVATLEBASG 540
Db 481 YEKQRETTYSTLTKTSTASINNLKPGTVVFOIRAVTAAGYGNYSPLDVATLEBASG 540
Qy 541 KMFEATAVSSQNPVITIAVAAGTIIIVMVFQIIIGRRHCGYSKADCGDEBELYFH 599
Db 541 KMFEATAVSSQNPVITIAVAAGTIIIVMVFQIIIGRRHCGYSKADCGDEBELYFH 599

RESULT 5
US-09-823-187-39
; Sequence 39, Application US/09823187
; Publication No. US20030096952A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine
; APPLICANT: Gueev, Vladimir Y
; APPLICANT: Liu, Xiaohong
; APPLICANT: Majumder, Kumud
; APPLICANT: Padigaru, Muralidhar
; APPLICANT: Paturajan, Meera
; APPLICANT: Shimkets, Richard A
; APPLICANT: Spaderma, Steven K
; APPLICANT: Spytek, Kimberly
; APPLICANT: Taudier, Raymond J
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-745
; CURRENT APPLICATION NUMBER: US/09/823,187
; PRIOR APPLICATION NUMBER: 60/193,339
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/193,205
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/195,343
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/195,088
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,005
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,792
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: 60/196,556
```

```
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: 60/197,081
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/197,525
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/197,087
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 993
; TYPE: PR
; ORGANISM: Gallus gallus
US-09-823-187-39
Query Match 90.8%; Score 3031.5; DB 10; Length 993;
Best Local Similarity 94.5%; Pred. No. 4,7e-231;
Matches 566; Conservative 17; Mismatches 11; Indels 5; Gaps 1;

Qy 1 MVOTRFPSPWIIICLYMLGFPAHTGEAQAKEVILLDSKAQOTELEWISSPPSGMEETISG 60
Db 1 MVOTRFPSPWIIICLYMLGFPAHTGEAQAKEVILLDSKAQOTELEWISSPPSGMEETISG 60
Qy 61 LDENVTPRTYOVQVQWNEPNNMRLTNWISKNAQRIFVELKFTLRDCLSPGLGTCK 120
Db 61 LDENVTPRTYOVQVQWNEPNNMRLTNWISKNAQRIFVELKFTLRDCLSPGLGTCK 120
Qy 121 ETFNLYYEETDYGGRNIRENLYVKIDITIADESFQDGLGERKMKLNTREIGPLSKK 180
Db 121 ETFNLYYEETDYGGRNIRENLYVKIDITIADESFQDGLGERKMKLNTREIGPLSKK 180
Qy 181 GFYLAPODVGACIALVSVKYYKKCWITVENLAVPDTVTGSEFSSLVEVRGTVCSSAEE 240
Db 181 GFYLAPODVGACIALVSVKYYKKCWITVENLAVPDTVTGSEFSSLVEVRGTVCSSAEE 240
Qy 241 EAENSPRMHCSAEGEWLVPIGKCIKAGYQOKGDTCEPCGRRFYKSSQDLQSCRCPHIS 300
Db 241 EAENSPRMHCSAEGEWLVPIGKCIKAGYQOKGDTCEPCGRRFYKSSQDLQSCRCPHIS 300
Qy 301 FSDREGSSRCCEDEGYRAPSDPPYVACTRPPSAQNLIENINOTTVSLFWSPPADNGCR 360
Db 301 FSDREGSSRCCEDEGYRAPSDPPYVACTRPPSAQNLIENINOTTVSLFWSPPADNGCR 360
Qy 361 NDVTYRILCKRCSEWQECVPCGSNIGMPQOTGLEDNVYTVMDLAAHAYTFEVEAVNG 420
Db 361 NDVTYRILCKRCSEWQECVPCGSNIGMPQOTGLEDNVYTVMDLAAHAYTFEVEAVNG 420
Qy 421 VSDLSRQRLFAAASITTGGAAPSOVSGWKEKRVLQRSVQELSWQEPHPNGVITEYEIKY 480
Db 421 VSDLSRQRLFAAASITTGGAAPSOVSGWKEKRVLQRSVQELSWQEPHPNGVITEYEIKY 480
Qy 481 YEKQRETTYSTLTKTSTASINNLKPGTVVFOIRAVTAAGYGNYSPLDVATLEBASG 540
Db 481 YEKQRETTYSTLTKTSTASINNLKPGTVVFOIRAVTAAGYGNYSPLDVATLEBASG 540
Qy 541 KMFEATAVSSQNPVITIAVAAGTIIIVMVFQIIIGRRHCGYSKADCGDEBELYFH 599
Db 540 ----ATAVSSQNPVITIAVAAGTIIIVMVFQIIIGRRHCGYSKADCGDEBELYFH 594

RESULT 6
US-09-823-187-41
; Sequence 41, Application US/09823187
; Publication No. US20030096952A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine
; APPLICANT: Gueev, Vladimir Y
; APPLICANT: Liu, Xiaohong
; APPLICANT: Majumder, Kumud
; APPLICANT: Padigaru, Muralidhar
; APPLICANT: Paturajan, Meera
; APPLICANT: Shimkets, Richard A
; APPLICANT: Spaderma, Steven K
```

APPLICANT: Spytek, Kimberly
APPLICANT: Taupier, Raymond J
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-745
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/193,339
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/193,205
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/195,343
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: 60/195,088
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,005
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,792
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: 60/196,556
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: 60/197,081
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 60/197,525
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/197,087
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 103
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 41
LENGTH: 993
TYPE: PRT
ORGANISM: Gallus gallus
US-09-823-187-41

Query Match 90.8%; Score 3031.5; DB 10; Length 993;
Best Local Similarity 94.5%; Pred. No. 4.7e-231;
Matches 566; Conservative 17; Mismatches 11; Indels 5; Gaps 1;
1 MVVORPSPWILTCYIMLGFAGTGEAOAKKEVLLDSKAQOTLEWISSPPSGMEETSG 60
1 MVLRSRLPFWMLGCVMLRFAHTGSAQAKSVILLDSKAQOTLEWISSPPSGMEETSG 60
61 LDENYPTRTYQVOCVMEBNONNMRLTNWISKGNARLFEVLKFTLRDONSIPVLTGTC 120
61 LDENYPTRTYQVOCVMEBNONNMRLTNWISKGNARLFEVLKFTLRDONSIPVLTGTC 120
121 ETEFNLYYETDYTGRIINRENLVKIDITIADESFQGDLSGRKKKLTVEVEIGPLSK 180
121 ETEFNLYYETDYTGRIINRENLVKIDITIADESFQGDLSGRKKKLTVEVEIGPLSK 180
121 ETEFNLYYETDYTGRIINRENLVKIDITIADESFQGDLSGRKKKLTVEVEIGPLSK 180
181 GFYLAFOVGACIALVSVKVVYKKKWTVENLAVFPDVTGSEFSLVEVRGTCVSSAE 240
181 GFYLAFOVGACIALVSVKVVYKKKWTVENLAVFPDVTGSEFSLVEVRGTCVSSAE 240
181 GFYLAFOVGACIALVSVKVVYKKKWTVENLAVFPDVTGSEFSLVEVRGTCVSSAE 240
241 EAENSPRMHCSAEGEMLVPIGKCIKAGYQKGDTCPCGRFRFYSSSODLQCSRCPTHS 300
241 EAENSPRMHCSAEGEMLVPIGKCIKAGYQKGDTCPCGRFRFYSSSODLQCSRCPTHS 300
241 EAENSPRMHCSAEGEMLVPIGKCIKAGYQKGDTCPCGRFRFYSSSODLQCSRCPTHS 300
301 FSDREGSSRCCEGDIYRAPSDPYVACTRPPSAPQNLIFINIQTTVSLWSPPADNGCR 360
301 FSDREGSSRCCEGDIYRAPSDPYVACTRPPSAPQNLIFINIQTTVSLWSPPADNGCR 360
301 FSDREGSSRCCEGDIYRAPSDPYVACTRPPSAPQNLIFINIQTTVSLWSPPADNGCR 360
361 NDVYTRILCKRCMSWQEGCVPGSGNIGWVPOOTGLVDNVTVMDLAANVFEVEANG 420
361 NDVYTRILCKRCMSWQEGCVPGSGNIGWVPOOTGLVDNVTVMDLAANVFEVEANG 420
361 NDVYTRILCKRCMSWQEGCVPGSGNIGWVPOOTGLVDNVTVMDLAANVFEVEANG 420
421 VSDLSRQRLFAVAISITTGQAAPSOVSGVMKERVLQRSVELSWSQEPHNGVITTEYIKY 480
421 VSDLSRQRLFAVAISITTGQAAPSOVSGVMKERVLQRSVELSWSQEPHNGVITTEYIKY 480
421 VSDLSRQRLFAVAISITTGQAAPSOVSGVMKERVLQRSVELSWSQEPHNGVITTEYIKY 480
481 YEKQDERTYSTLTKKTSASINNLKPGTVVYFOIRAVTAAGYGYSPRLDVATLEASG 540
481 YEKQDERTYSTLTKKTSASINNLKPGTVVYFOIRAVTAAGYGYSPRLDVATLEASG 540
481 YEKQDERTYSTLTKKTSASINNLKPGTVVYFOIRAVTAAGYGYSPRLDVATLEASG 540

541 KMFETAVSSSEONPIIIIAVAVAGTILVFMVFGFIIGRRHCGYSKADQGEDELYTH 599
540 -----ATAVSEONPIIIIAVAVAGTILVFMVFGFIIGRRHCGYSKADQGEDELYTH 594

RESULT 7
US-09-823-187-44
Sequence 44, Application US/09823187
Publication NO. US20030096952A1
GENERAL INFORMATION:
APPLICANT: Burgess, Catherine
APPLICANT: Gusev, Vladimir Y
APPLICANT: Liu, Xiaohong
APPLICANT: Majumder, Kunud
APPLICANT: Padigaru, Muralidhar
APPLICANT: Patuturajan, Meera
APPLICANT: Shinkels, Richard A
APPLICANT: Spaderna, Steven K
APPLICANT: Spytek, Kimberly
APPLICANT: Taupier, Raymond J
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-745
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/193,339
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/193,205
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/195,343
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: 60/195,088
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,005
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,792
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: 60/196,556
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: 60/197,081
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 60/197,525
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/197,087
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 103
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 44
LENGTH: 991
TYPE: PRT
ORGANISM: Homo sapiens
US-09-823-187-44

Query Match 55.2%; Score 1841; DB 10; Length 991;
Best Local Similarity 57.4%; Pred. No. 1.2e-136;
Matches 345; Conservative 97; Mismatches 133; Indels 26; Gaps 8;
6 RPPSW--IILCYIMLGFAGTGEAOAKKEVLLDSKAQOTLEWISSPPSGMEETSG 63
6 RPPSW--IILCYIMLGFAGTGEAOAKKEVLLDSKAQOTLEWISSPPSGMEETSG 63
13 RAPLWTCILLC-----ALRFTLASPSNEVNLDSRTVMGDLGWIAPKNGMEETGEVDE 67
13 RAPLWTCILLC-----ALRFTLASPSNEVNLDSRTVMGDLGWIAPKNGMEETGEVDE 67
64 NYTPRTYQVOCVMEBNONNMRLTNWISKGNARLFEVLKFTLRDONSIPVLTGTCETP 123
64 NYTPRTYQVOCVMEBNONNMRLTNWISKGNARLFEVLKFTLRDONSIPVLTGTCETP 123
68 NYAPHTYQVOCVMEBNONNMRLTNWISKGNARLFEVLKFTLRDONSIPVLTGTCETP 127
68 NYAPHTYQVOCVMEBNONNMRLTNWISKGNARLFEVLKFTLRDONSIPVLTGTCETP 127
124 NLVYETDYTGRIINRENLVKIDITIADESFQGDLSGRKKKLTVEVEIGPLSKGKY 183
124 NLVYETDYTGRIINRENLVKIDITIADESFQGDLSGRKKKLTVEVEIGPLSKGKY 183
128 NMVYFESDQNGRINKENQYIKIDITIADESFTELDGRVWKLTVEVRDVGPLSKGKY 187
128 NMVYFESDQNGRINKENQYIKIDITIADESFTELDGRVWKLTVEVRDVGPLSKGKY 187
184 LAFQDVGACIALVSVKVVYKKKWTVENLAVFPDVTGSEFSLVEVRGTCVSSAEAEAE 243
184 LAFQDVGACIALVSVKVVYKKKWTVENLAVFPDVTGSEFSLVEVRGTCVSSAEAEAE 243
188 LAFQDVGACIALVSVKVVYKKKWTVENLAVFPDVTGSEFSLVEVRGTCVSSAEAEAE 245
188 LAFQDVGACIALVSVKVVYKKKWTVENLAVFPDVTGSEFSLVEVRGTCVSSAEAEAE 245


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Db      239 RPPSAARPAISNVNNTSVLEMI PPADTGRGDVSYIAACKCKNSHAGCECGHVRLL 358
Qy      390 POOTGLJDNVYVMDLLAHANTFPEAVANGVSDLSRSQRLFAAVSITGGAAPSOVGV 449
Db      339 PROSLKTKTSVMMVLLAHTNTTTEIEAVANGVSDLSPGARQYVAVVITNOAPSEVITV 418
Qy      450 MKERVLORSVOLSWOEPHEHNVITEYEIKYEEKQDERTYSTLTKTSASINNLKPGT 509
Db      419 KKGKIAKNSISLSWQEPDRPNCIILEYEIKHFEKQD-ETSYITIKSKETTITABGLKPAS 477
Qy      510 VYVFOIRAVTAAGYGNYSRDLVALTEASGKMFAT---AVSSEQNPVITIAVAVAGT 566
Db      478 VYVFOIRATAAGYGFSSRRFE-----FETTPVFAASDOSQIPVIAVSVTVG- 525
Qy      567 IIVFMVGFIIIGRRHCGYSKADQSGDEE-LYFHS 600
Db      526 VILLAVIGVILSGRRCGYSKAKQDPEEKMHFN 560

```

RESULT 10

```

US-10-732-923-13667
; Sequence 13667, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgeton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO: 13667
; LENGTH: 991
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-732-923-13667

```

Query Match 54.7%; Score 1827; DB 17; Length 991;

Best Local Similarity 58.0%; Pred. No. 1.5e-135;

Matches 346; Conservative 95; Mismatches 134; Indels 22; Gaps 8;

```

Qy      8 PSM--IILCYWILGFAHTGEAQAKEVLLDLSKAQOTLEWISSPPSGMEISGLDENV 65
Db      15 PGMTCILLCALRLSLASPG-----SEVLLDSRTYMGDLGMIAPKNGMEIIGVDENY 69
Qy      66 TPRTYQVQVNEPQNNMLRTNWSKGNARIIVELKFTLRDCNSLPGLGTCKETPNL 125
Db      70 AFIHTYQVCKWQEQNNMLLTSMISNEGRPASSPELKFTLRDCNSLPGLGTCKETPNM 129
Qy      126 YYYEFDYDTGRNIRENLYKIDITIADESFTOGDIGERKMKLNTVEIREIGLSKGFYLA 185
Db      130 YFESDDEDEGRNIRENOYIKIDITIADESFTELDGRVWKLNTEVRDVGPLTKGPFYLA 189
Qy      166 PDVAGACIALVAVKYKKCWITIVENTLAVPPDTVSGSESSLVEVRGTVS--SABEAEAN 244
Db      190 PDVAGACIALVAVRYKKCPSVIRGLAFPPDTITGADSSQLLEVSAGVNVNSVTDEA-- 247
Qy      245 SPRMCSAGEWLVPIGKICIKAGYQOKGDTCEPCGRFRFYKSSODLQCSRPPTSHFSDR 304
Db      248 -PKMCSAGEWLVPIGKLCCKAGYEKNNTQVCRPGFKASPHSPSCSKPPHSYITLD 306
Qy      305 EGSSRCECEGDGYRAPSDPPYACTRPPAPQNLIFINQTTVSLWSPAPANGGANDVT 364
Db      307 EASTCLCEEHYFRRESDDPTMACTRPPAPSAISNVETSVFLEWIPAPDTGGRKDV 366
Qy      365 YVILCKRGWEGECVPCGSGNIGVMPQOTGLJDNVYVMDLLAHANTFPEAVANGVSD 424
Db      367 YVILCKKSHSGLCACGSHVRYLPQOGLKNTSVWMDLAAHTNTTTEIEAVANGVSD 426
Qy      425 SRSORLFAAVSITGGAAPSOVSGVWKEVLORSVOLSWOEPHEHNVITEYEIKYEEKD 484

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Db      427 NPGARQVSVVNTNOAPSPSVSYKCKITKNISLSWQEPDRPNCIILEYEIKYEEKD 486
Qy      485 QERTYSTLTKTSASINNLKPGTVYVFOIRAVTAAGYGNYSRDLVALTEASGKMFAT 544
Db      487 Q-ETSYITIKSKETTITABGLKPASAVYVFOIRARAAGYGFSSRRFEET-----SP 537
Qy      545 ATAVSSEQNPVITIAVAVAGTIIIVFMVGFIIIGRRHCGYSKADQSGDEE-LYFHS 600
Db      538 VLAASDQSQPII-VVSVTVGIVILLAVIGFLLSGRRCGYSKAKQDPEEKMHFN 593

```

RESULT 11

```

US-10-029-020-63
; Sequence 63, Application US/10029020
; Publication No. US20040033971A1
; GENERAL INFORMATION:
; APPLICANT: Gangoli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/10/029,020
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 63
; LENGTH: 1005
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-029-020-63

```

Query Match 54.5%; Score 1819; DB 15; Length 1005;

Best Local Similarity 55.1%; Pred. No. 6.6e-135;

Matches 348; Conservative 96; Mismatches 136; Indels 52; Gaps 10;

```

Qy      6 RPPSMIILCY-----IIV---LIGFAHTGEAQAKEVLLDLSKAQOTLEWISSPPSG 54
Db      25 RVPASLACYSAPLKGPMITCLLCALRLTLASPSNVNLLDSRTVLDGMIAPKNG 84
Qy      55 WEISGLDENVTPRTYQVQVNEPQNNMLRTNWSKGNARIIVELKFTLRDCNSLP 114
Db      85 WEISEVDENTAFLHTYQVCKWQEQNNMLLTSMISNEGRSRIPELKFTLRDCNSLP 144
Qy      115 VLGTCKETPNLYYYETDYDTGRNIRENLYKIDITIADESFTOGDIGERKMKLNTVEIR 174
Db      145 GLGTCKETPNMYYPESDDENGRNIDKNQYIKIDITIADESFTELDGRVWKLNTEVRDV 204
Qy      175 GPLSKGYYLAFQDYGACIALVAVKYKKCWITIVENTLAVPPDTYTGSEFSLVVRGTC 234
Db      205 GPLSKGYYLAFQDYGACIALVAVRYKKCPSVIRGLAFPPDTITGADSSQLLEVSQC 264
Qy      235 VSSAEBEABNSPRMCSAGEWLVPIGKICIKAGYQOKGDTCEPCGRFRFYKSSODLQCS 294
Db      265 VV--HSVTDDEPKMCSAGEWLVPIGKCKAGYEKNNGTCQVCRPGFKASPHSQC 322
Qy      295 RCPTHSFDRGSSRCECEGDGYRAPSDPPYACTRPPAPQNLIFINQTTVSLWSP 354

```


Db 323 KCPHSTHHEASTSCVCEKDYFRRESPPPTMACTRPPSAPRNAISVNTSVLEMTIP 382
Qy 355 ADNGRNDVYRIILCKRCSWEGECVPCGSNIYMPOQTGLEJNYVMDLAAHANYTPE 414
Db 333 ADTGCKGVASYIILCKKCNHAGVCECGHVRYPQDILKNTSVWMDLAAHANYTPE 442
Qy 415 VEAVNGVSDLSRQSLFPAVSTTTGGAAPSOVSGWKEKRVLORSVOLSWQEPHNGYIT 474
Db 443 IEAVNGVSDLSRQSLFPAVSTTTGGAAPSOVSGWKEKRVLORSVOLSWQEPHNGYIT 502
Qy 475 EYEIYKEDORERTYSTLTKTSTASINNLKPGTVYVFOIRAVTAAGVNSPRLDVAT 534
Db 503 EYEIYKEDORERTYSTLTKTSTASINNLKPGTVYVFOIRAVTAAGVNSPRLDVAT 558
Qy 535 LEASGKMEATAV---SSEQNPVILIAVAVAGTIIIVFWGFI-----GRR- 581
Db 559 -----FETTPVGAANDSQPIIIGVSVTVGILLAVMI-GLLSG3CCECGGRAS 609
Qy 582 -----HCGYSKADQEGDEE-LYFHS 600
Db 610 SLCAVAHPSLIWRCGYSKAKODPEEEKMHFN 641

RESULT 12
US-10-316-124-3
; Sequence 3, Application US/10316124
; Publication No. US20030152574A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: METHODS AND COMPOSITIONS TO TREAT
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1419, 58765, AND 2210
; FILE REFERENCE: MP101-291P1RM
; CURRENT APPLICATION NUMBER: US/10/316,124
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/339,995
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1037
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-316-124-3

Query Match 54.4%; Score 1817; DB 14; Length 1037;
Best Local Similarity 55.5%; Pred. No. 1e-134;
Matches 346; Conservative 97; Mismatches 132; Indels 48; Gaps 10;

Qy 6 RPPSW--ILCYIWLGFHAHTGEAQAKEVILLDSKAQOTELEWISSPP3GMEETISGLDE 63
Db 37 RAPLWTCILLC-----AALRTILASPSNEVNLDSRTVGDGLGWIAPKNGMEETIGEVDE 91
Qy 64 NYTPRTYQVQVQWEPNOMNMLRTWISKNAQRIFVFLKTLTLDNSL3VGLGCKETTF 123
Db 92 NYAPHTYQVQVQWEPNOMNMLRTWISKNAQRIFVFLKTLTLDNSL3VGLGCKETTF 151
Qy 124 NLYYETDYDGRNIRENLYVYKIDITIADESFTQDGLERKMKLNTETVRI3GPLSKGIFY 183
Db 152 NMYYESDQNGRINKENQYIKIDITIADESFTEDLDGRWKLNTETVRI3GPLSKGIFY 211
Qy 184 LAFQDVGAALVSVKYVYKTCMTIVENLAVFPDITVTSSEFSSLVEVRG7CVSSAEEBAE 243
Db 212 LAFQDVGAALVSVKYVYKTCMTIVENLAVFPDITVTSSEFSSLVEVRG7CVSSAEEBAE 269
Qy 244 NSPRMHGAEGBMLVPIKCLICAGYQOKDTCCEGGRFPYKSSSQDQC3SRCPHSSSD 303
Db 270 EPPKMHGAEGBMLVPIKCLICAGYQOKDTCCEGGRFPYKSSSQDQC3SRCPHSSSD 329
Qy 304 REGSRCECDGYVAPSDPPYVACTRPPSAPONLIIFINOTTVSLEWS3PADNGGRNDV 363
Db 330 EEAISTCVCEKDYFRRESPPPTMACTRPPSAPRNAISVNTSVLEMTIP3ADTGCKGV 389

Qy 364 TYRILCKRCSWEGECVPCGSNIYMPOQTGLEJNYVMDLAAHANYTPEVAVNGVSD 423
Db 390 SYYLACKKCNHAGVCECGHVRYPQDILKNTSVWMDLAAHANYTPEIEAVNGVSD 449
Qy 424 LSRQSLFPAVSTTTGGAAPSOVSGWKEKRVLORSVOLSWQEPHNGYIT 483
Db 450 LSPARQVSVNVTNQAAPSPVTNVKKGKIAKNSISLSWOEPDRPGIILEYIKFKEK 509
Qy 484 DQERERTYSTLTKTSTASINNLKPGTVYVFOIRAVTAAGVNSPRLDVATLEASGKMF 543
Db 510 DQ-ERTYSTLTKTSTASINNLKPGTVYVFOIRAVTAAGVNSPRLDVATLEASGKMF 557
Qy 544 EAT---AVSEQNPVILIAVAVAGTIIIVFWGFI-----GRR- 581
Db 558 ETTVPFASSDQSGIPIVAVSVTG-VILLAVTVGILLSG8CCECGGRASSLCAVAHPI 616
Qy 582 ---HCGYSKADQEGDEE-LYFHS 600
Db 617 LWRGYSKAKODPEEEKMHFN 639

RESULT 13
US-10-353-690-40
; Sequence 40, Application US/10353690
; Publication No. US20030215840A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Miyoung
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Healy, Aileen
; APPLICANT: Accion, Susan L.
; APPLICANT: Donoghue, Mary
; APPLICANT: Stagliano, Nancy
; APPLICANT: Perodini, Jacqueline
; APPLICANT: Rodrique-Way, Amelie
; TITLE OF INVENTION: Methods and compositions for treating
; TITLE OF INVENTION: cardiovascular disease using 1682, 6169, 6193, 7771, 14395,
; TITLE OF INVENTION: 29002, 33216, 43726, 69292, 26156, 32427, 2402, 7747, 1720,
; TITLE OF INVENTION: 9151, 60491, 1371, 7077, 33207, 1419, 18036, 16105, 38650,
; TITLE OF INVENTION: 14245, 58848, 1870, 25856, 32394, 3484, 345, 9252, 9135,
; TITLE OF INVENTION: 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912, 2868,
; TITLE OF INVENTION: 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914,
; TITLE OF INVENTION: 51130, 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474,
; FILE REFERENCE: MP102-018P1RNMNIM
; CURRENT APPLICATION NUMBER: US/10/353,690
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 60/353,224
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/364,529
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: 60/373,861
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/376,287
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 60/388,080
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: 60/390,971
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/394,130
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/394,797
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/404,904
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 60/405,450
; PRIOR FILING DATE: 2002-08-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 1037
; TYPE: PRT

ORGANISM: Homo Sapiens
US-10-353-690-40

Query Match 54.4%; Score 1817; DB 15; Length 1037;

Best Local Similarity 55.5%; Pred. No. 1e-134; Indels 48; Gaps 10;

Matches 346; Conservative 97; Mismatches 132;

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6 RPSW--IILCYIWLGFHATGEAOAKEVLLDLSKAQTELEWISSPPSGMEISGIDE 63
37 RAPLMTCLLC-----AALRTLLASPSNEVNLDSRTVMGDLGWIAFPMNGMEIEGVIDE 91
64 NTPPIRTYQVQWMEPNONNMLRTNWSKGAQRI FVELKFTLRDONSIPVGLGCKETF 123
92 NYAPIHTYQVCKVMEQONNNMLTWSISNEGASRI FIELKFTLRDONSIPGLGCKETF 151
124 NLYYETDYDGRNIRENLYYKIDITIADESFTOGDLGERKMKLNTVEIRIGPLSKGPFY 183
152 NMYYESDDQNGRNIRKENQYIKIDITIADESFTELDDGRVMKLTVEIRDVGLSKGPFY 211
184 LAFQDVGACIALVSRYVYKKCWITIVENLAVFPDVTGSEFSLVEVRGTCVSAEEBAE 243
212 LAFQDVGACIALVSRYVYKKCWITIVENLAVFPDVTGSEFSLVEVRGTCVSAEEBAE 269
244 NSPRMHCAGEBMLVPIGKCIKAGYQOKGDTCEPCGRFRFYKSSQDLQCSRCPHSTFS 303
270 EPPKMGCSAGEBMLVPIGKCMCKAGYEEKNGTCQVCRPGFKAAPHIOSCGKCPHSTYH 329
304 REGSRCECEQGYRAPSDPPYVACTRPPSAFONLI FPNINQTVSLEWSPPADNGGRUDV 363
330 BEASTSCVCEKDYFRRESDPPTMACTRPPSAPRNAINSVNETSVLEIIPPADTGGKRDV 389
364 TYRILCKRCSMEQECVPCGSGNIGYMPQOTGLEEDNYVTMDLAAHANTFEVEAVNGSD 423
390 SYTIACKCKNSHAGVCECGHVRILPROSGIKNTSVMMVDLANTTTFEIEAVNGSD 449
424 LRSORLFAVSIITGGAAPSOVSGMKERYLQSVLSMOBPEHPNVTIEYEIKYEEK 483
450 LSPGARQYVAVNTTNOAPSPVTNVKKGKIAKNSISLSWQEPDRPNGLILEYEIKHEK 509
484 DORERTYTLTKTSASINNLKPGTVYVFOIRAVTAAGYGNYSRLDVATLEASGMF 543
510 DQ-ETSYIIISKETTTIABGLKPASVYVFOIRAVTAAGYGVFSRFE-----F 557
544 EAT---AVSSEONPVIIIAVAVAGTIIIVMVFEGFI-----GRR----- 581
558 ETPPFAASSDQSQIPVIAVSVTVG-VILLAVIGVLLSGSCCEGCGRASSLCAVAHPI 616
582 ---HCGYSKADQEGDEE-LYFHS 600
617 LIWRCGYSKAKQDPDEEEMHFFHN 639

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RESULT 14
US-11-064-551-3

Sequence 3, Application US/11064551

Publication No. US20050142604A1

GENERAL INFORMATION:

APPLICANT: Logan, Thomas Joseph

APPLICANT: Chun, Miyoung

TITLE OF INVENTION: METHODS AND COMPOSITIONS TO TREAT

FILE REFERENCE: MP101-291P1RM

CURRENT FILING DATE: 2005-02-24

PRIOR FILING DATE: 2001-12-10

NUMBER OF SEQ ID NOS: 9

SOFTWARE: FastSeq for Windows Version 4.0

Query Match 54.4%; Score 1817; DB 20; Length 1037;

Best Local Similarity 55.5%; Pred. No. 1e-134; Indels 48; Gaps 10;

Matches 346; Conservative 97; Mismatches 132;

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6 RPSW--IILCYIWLGFHATGEAOAKEVLLDLSKAQTELEWISSPPSGMEISGIDE 63
37 RAPLMTCLLC-----AALRTLLASPSNEVNLDSRTVMGDLGWIAFPMNGMEIEGVIDE 91
64 NTPPIRTYQVQWMEPNONNMLRTNWSKGAQRI FVELKFTLRDONSIPVGLGCKETF 123
92 NYAPIHTYQVCKVMEQONNNMLTWSISNEGASRI FIELKFTLRDONSIPGLGCKETF 151
124 NLYYETDYDGRNIRENLYYKIDITIADESFTOGDLGERKMKLNTVEIRIGPLSKGPFY 183
152 NMYYESDDQNGRNIRKENQYIKIDITIADESFTELDDGRVMKLTVEIRDVGLSKGPFY 211
184 LAFQDVGACIALVSRYVYKKCWITIVENLAVFPDVTGSEFSLVEVRGTCVSAEEBAE 243
212 LAFQDVGACIALVSRYVYKKCWITIVENLAVFPDVTGSEFSLVEVRGTCVSAEEBAE 269
244 NSPRMHCAGEBMLVPIGKCIKAGYQOKGDTCEPCGRFRFYKSSQDLQCSRCPHSTFS 303
270 EPPKMGCSAGEBMLVPIGKCMCKAGYEEKNGTCQVCRPGFKAAPHIOSCGKCPHSTYH 329
304 REGSRCECEQGYRAPSDPPYVACTRPPSAFONLI FPNINQTVSLEWSPPADNGGRUDV 363
330 BEASTSCVCEKDYFRRESDPPTMACTRPPSAPRNAINSVNETSVLEIIPPADTGGKRDV 389
364 TYRILCKRCSMEQECVPCGSGNIGYMPQOTGLEEDNYVTMDLAAHANTFEVEAVNGSD 423
390 SYTIACKCKNSHAGVCECGHVRILPROSGIKNTSVMMVDLANTTTFEIEAVNGSD 449
424 LRSORLFAVSIITGGAAPSOVSGMKERYLQSVLSMOBPEHPNVTIEYEIKYEEK 483
450 LSPGARQYVAVNTTNOAPSPVTNVKKGKIAKNSISLSWQEPDRPNGLILEYEIKHEK 509
484 DORERTYTLTKTSASINNLKPGTVYVFOIRAVTAAGYGNYSRLDVATLEASGMF 543
510 DQ-ETSYIIISKETTTIABGLKPASVYVFOIRAVTAAGYGVFSRFE-----F 557
544 EAT---AVSSEONPVIIIAVAVAGTIIIVMVFEGFI-----GRR----- 581
558 ETPPFAASSDQSQIPVIAVSVTVG-VILLAVIGVLLSGSCCEGCGRASSLCAVAHPI 616
582 ---HCGYSKADQEGDEE-LYFHS 600
617 LIWRCGYSKAKQDPDEEEMHFFHN 639

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RESULT 15
US-10-412-277-8

Sequence 8, Application US/10412277

Publication No. US20030175791A1

GENERAL INFORMATION:

APPLICANT: GUEGLER, Karl et al

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

FILE REFERENCE: C1001067DIV

CURRENT FILING DATE: 2003-04-14

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 8

LENGTH: 975

TYPE: PRT

Query Match 54.1%; Score 1806.5; DB 14; Length 975;

Best Local Similarity 56.8%; Pred. No. 6.2e-134; Indels 41; Gaps 8;

Matches 339; Conservative 95; Mismatches 122;

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6 RPSW--IILCYIWLGFHATGEAOAKEVLLDLSKAQTELEWISSPPSGMEISGIDE 63
37 RAPLMTCLLC-----AALRTLLASPSNEVNLDSRTVMGDLGWIAFPMNGMEIEGVIDE 91
64 NTPPIRTYQVQWMEPNONNMLRTNWSKGAQRI FVELKFTLRDONSIPVGLGCKETF 123
92 NYAPIHTYQVCKVMEQONNNMLTWSISNEGASRI FIELKFTLRDONSIPGLGCKETF 151
124 NLYYETDYDGRNIRENLYYKIDITIADESFTOGDLGERKMKLNTVEIRIGPLSKGPFY 183
152 NMYYESDDQNGRNIRKENQYIKIDITIADESFTELDDGRVMKLTVEIRDVGLSKGPFY 211
184 LAFQDVGACIALVSRYVYKKCWITIVENLAVFPDVTGSEFSLVEVRGTCVSAEEBAE 243
212 LAFQDVGACIALVSRYVYKKCWITIVENLAVFPDVTGSEFSLVEVRGTCVSAEEBAE 269
244 NSPRMHCAGEBMLVPIGKCIKAGYQOKGDTCEPCGRFRFYKSSQDLQCSRCPHSTFS 303
270 EPPKMGCSAGEBMLVPIGKCMCKAGYEEKNGTCQVCRPGFKAAPHIOSCGKCPHSTYH 329
304 REGSRCECEQGYRAPSDPPYVACTRPPSAFONLI FPNINQTVSLEWSPPADNGGRUDV 363
330 BEASTSCVCEKDYFRRESDPPTMACTRPPSAPRNAINSVNETSVLEIIPPADTGGKRDV 389
364 TYRILCKRCSMEQECVPCGSGNIGYMPQOTGLEEDNYVTMDLAAHANTFEVEAVNGSD 423
390 SYTIACKCKNSHAGVCECGHVRILPROSGIKNTSVMMVDLANTTTFEIEAVNGSD 449
424 LRSORLFAVSIITGGAAPSOVSGMKERYLQSVLSMOBPEHPNVTIEYEIKYEEK 483
450 LSPGARQYVAVNTTNOAPSPVTNVKKGKIAKNSISLSWQEPDRPNGLILEYEIKHEK 509
484 DORERTYTLTKTSASINNLKPGTVYVFOIRAVTAAGYGNYSRLDVATLEASGMF 543
510 DQ-ETSYIIISKETTTIABGLKPASVYVFOIRAVTAAGYGVFSRFE-----F 557
544 EAT---AVSSEONPVIIIAVAVAGTIIIVMVFEGFI-----GRR----- 581
558 ETPPFAASSDQSQIPVIAVSVTVG-VILLAVIGVLLSGSCCEGCGRASSLCAVAHPI 616
582 ---HCGYSKADQEGDEE-LYFHS 600
617 LIWRCGYSKAKQDPDEEEMHFFHN 639

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RESULT 15
US-10-412-277-8

Sequence 8, Application US/10412277

Publication No. US20030175791A1

GENERAL INFORMATION:

APPLICANT: GUEGLER, Karl et al

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

FILE REFERENCE: C1001067DIV

CURRENT FILING DATE: 2003-04-14

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 8

LENGTH: 975

TYPE: PRT

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 23, 2005, 08:26:40 ; Search time 21.7783 Seconds
(without alignments) 2145.727 Million cell updates/sec

Title: US-10-073-064-5
Perfect score: 3338
Sequence: 1 MVVQTRRPSWILLCYWILG.....DMEKTOHKKMVIASCSRL 626

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*\n2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*\n3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*\n4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*\n5: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep:*\n6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----------------------|--------------------|
| 1 | 3338 | 100.0 | 626 | 3 US-08-368-776A-5 | Sequence 5, Appl1 |
| 2 | 3338 | 100.0 | 626 | PCT-US96-00419-5 | Sequence 5, Appl1 |
| 3 | 3199 | 95.8 | 610 | 3 US-08-368-776A-3 | Sequence 3, Appl1 |
| 4 | 3199 | 95.8 | 610 | PCT-US96-00419-3 | Sequence 3, Appl1 |
| 5 | 3191.5 | 95.6 | 994 | 3 US-08-368-776A-12 | Sequence 12, Appl1 |
| 6 | 3191 | 95.6 | 998 | 3 US-08-368-776A-2 | Sequence 2, Appl1 |
| 7 | 3191 | 95.6 | 998 | PCT-US96-00419-2 | Sequence 2, Appl1 |
| 8 | 3151.5 | 94.4 | 993 | 3 US-08-368-776A-11 | Sequence 11, Appl1 |
| 9 | 3139 | 94.0 | 998 | 2 US-08-449-645A-17 | Sequence 17, Appl1 |
| 10 | 3139 | 94.0 | 998 | 2 US-08-702-367A-17 | Sequence 17, Appl1 |
| 11 | 3139 | 94.0 | 998 | 4 US-09-949-016-6501 | Sequence 6501, Ap |
| 12 | 3139 | 94.0 | 998 | PCT-US95-04681-17 | Sequence 17, Appl1 |
| 13 | 3139 | 94.0 | 1005 | 4 US-09-949-016-9901 | Sequence 9901, Ap |
| 14 | 1841 | 55.2 | 991 | 2 US-08-449-645A-13 | Sequence 13, Appl1 |
| 15 | 1841 | 55.2 | 991 | 2 US-08-702-367A-13 | Sequence 13, Appl1 |
| 16 | 1841 | 55.2 | 991 | PCT-US95-04681-13 | Sequence 13, Appl1 |
| 17 | 1833.5 | 54.9 | 967 | 2 US-08-449-645A-30 | Sequence 30, Appl1 |
| 18 | 1833.5 | 54.9 | 967 | 2 US-08-702-367A-30 | Sequence 30, Appl1 |
| 19 | 1830.5 | 54.8 | 953 | 4 US-09-751-389-7 | Sequence 7, Appl1 |
| 20 | 1822 | 54.6 | 1005 | 4 US-08-469-537A-103 | Sequence 103, App |
| 21 | 1806.5 | 54.1 | 975 | 4 US-09-751-389-8 | Sequence 8, Appl1 |
| 22 | 1790 | 53.6 | 983 | 1 US-08-167-919A-10 | Sequence 10, Appl1 |
| 23 | 1790 | 53.6 | 983 | 2 US-08-449-645A-21 | Sequence 21, Appl1 |
| 24 | 1790 | 53.6 | 983 | 2 US-08-702-367A-21 | Sequence 21, Appl1 |
| 25 | 1790 | 53.6 | 983 | 3 US-08-715-106-10 | Sequence 10, Appl1 |
| 26 | 1790 | 53.6 | 983 | 4 US-09-442-649-10 | Sequence 10, Appl1 |
| 27 | 1790 | 53.6 | 983 | 5 PCT-US95-04681-21 | Sequence 21, Appl1 |

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| 28 | 1783.5 | 53.4 | 968 | 4 US-09-751-389-6 | Sequence 6, Appl1 |
| 29 | 1776 | 53.2 | 982 | 2 US-08-673-789-4 | Sequence 4, Appl1 |
| 30 | 1775.5 | 53.2 | 983 | 1 US-08-162-809-16 | Sequence 16, Appl1 |
| 31 | 1741.5 | 52.2 | 986 | 2 US-08-449-645A-15 | Sequence 15, Appl1 |
| 32 | 1741.5 | 52.2 | 986 | 2 US-08-702-367A-15 | Sequence 15, Appl1 |
| 33 | 1741.5 | 52.2 | 986 | 5 PCT-US95-04681-15 | Sequence 15, Appl1 |
| 34 | 1741.5 | 52.2 | 997 | 4 US-09-949-016-7171 | Sequence 7171, Ap |
| 35 | 1734.5 | 52.0 | 1104 | 1 US-08-222-616-36 | Sequence 36, Appl1 |
| 36 | 1734.5 | 52.0 | 1104 | 3 US-08-446-648-36 | Sequence 36, Appl1 |
| 37 | 1734.5 | 52.0 | 1104 | 4 US-09-982-610-36 | Sequence 36, Appl1 |
| 38 | 1734.5 | 52.0 | 1104 | 5 PCT-US95-04228-36 | Sequence 36, Appl1 |
| 39 | 1734 | 51.9 | 986 | 2 US-08-673-789-3 | Sequence 3, Appl1 |
| 40 | 1701.5 | 51.0 | 1005 | 4 US-09-949-016-6968 | Sequence 6968, Ap |
| 41 | 1701.5 | 51.0 | 1005 | 4 US-09-949-016-10620 | Sequence 10620, A |
| 42 | 1665.5 | 49.9 | 1036 | 4 US-09-751-389-2 | Sequence 2, Appl1 |
| 43 | 1661.5 | 49.8 | 942 | 4 US-10-004-542-2 | Sequence 2, Appl1 |
| 44 | 1661.5 | 49.8 | 942 | 4 US-10-430-797-2 | Sequence 2, Appl1 |
| 45 | 1655 | 49.6 | 948 | 2 US-08-469-537A-101 | Sequence 101, App |

ALIGNMENTS

RESULT 1
US-08-368-776A-5
: Sequence 5, Application US/08368776A
: Patent No. 6306482
: GENERAL INFORMATION:
: APPLICANT: Closser, Thomas
: APPLICANT: Ullrich, Axel
: APPLICANT: Millaer, Birgit
: TITLE OF INVENTION: METHODS FOR DIAGNOSIS
: TITLE OF INVENTION: AND TREATMENT OF MDK1
: TITLE OF INVENTION: SIGNAL TRANSDUCTION
: TITLE OF INVENTION: DISORDERS
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Lyon & Lyon
: STREET: 633 West Fifth Street
: STREET: Suite 4700
: CITY: Los Angeles
: STATE: California
: COUNTRY: U.S.A.
: ZIP: 90071-2066
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5" Diskette, 1.44 MB
: MEDIUM TYPE: Storage
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: IBM P.C. DOS 5.0
: SOFTWARE: Word Perfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/368, 776A
: FILING DATE: January 3, 1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: PRIOR APPLICATION DATA: including application
: APPLICATION NUMBER: described below:
: none
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Warburg, Richard J.
: REGISTRATION NUMBER: 32,327
: REFERENCE/DOCKET NUMBER: 208/007
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (213) 489-1600
: TELEFAX: (213) 955-0440
: TELEX: 67-3510
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 626 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-368-776A-5

Query Match 100.0%; Score 3338; DB 3; Length 626;
Best Local Similarity 100.0%; Pred. No. 1.3e-298;
Matches 626; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MVTQTRFSPSWIIICYYIMLGFPAHTGEAQAKEYLLDSKAQTELEWISSPPSGMEISG 60
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DB 1 MVTQTRFSPSWIIICYYIMLGFPAHTGEAQAKEYLLDSKAQTELEWISSPPSGMEISG 60
QY 61 LDENYPIRTYQYQCVMEPNQNNWLRTNWSKGNARIFVELKFTLSDCNSLPGVLTGCK 120
    |||
DB 61 LDENYPIRTYQYQCVMEPNQNNWLRTNWSKGNARIFVELKFTLSDCNSLPGVLTGCK 120
QY 121 EFTENLYYEETDYDTGNIRRENLYVKIDTIADESFTQDGLGERKMKLNTVEIRIGPLSKK 180
    |||
DB 121 EFTENLYYEETDYDTGNIRRENLYVKIDTIADESFTQDGLGERKMKLNTVEIRIGPLSKK 180
QY 181 GFYLAFOVDGACIALVSVKYKKKWTIVENLAVFPDVTGSEFSSLVEVRGTCVSSAEE 240
    |||
DB 181 GFYLAFOVDGACIALVSVKYKKKWTIVENLAVFPDVTGSEFSSLVEVRGTCVSSAEE 240
QY 241 EAENSPPRMCSAAGEMLVPIGKICIKAGYQOKGDTCEPCGRRRYKSSSDLOCSRCPHIS 300
    |||
DB 241 EAENSPPRMCSAAGEMLVPIGKICIKAGYQOKGDTCEPCGRRRYKSSSDLOCSRCPHIS 300
QY 301 FSDREGSSRCECEDGYRRAPSDPPYACTRPPSAPQNLFININQTTVLSLWSPADNGR 360
    |||
DB 301 FSDREGSSRCECEDGYRRAPSDPPYACTRPPSAPQNLFININQTTVLSLWSPADNGR 360
QY 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQOTGLENDYVTWDLAAHANYFEVEAVNG 420
    |||
DB 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQOTGLENDYVTWDLAAHANYFEVEAVNG 420
QY 421 VSDLSRQRLFAAVSTTGAAPSQVSGWKERYLQRSVOLSQOEPHEHPGVITTEYIKY 480
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DB 421 VSDLSRQRLFAAVSTTGAAPSQVSGWKERYLQRSVOLSQOEPHEHPGVITTEYIKY 480
QY 481 YEKDQERRTYTLTKTSTASINNLKPGTYVFOIRAVTAAGYNSPRLDVAITLLEASG 540
    |||
DB 481 YEKDQERRTYTLTKTSTASINNLKPGTYVFOIRAVTAAGYNSPRLDVAITLLEASG 540
QY 541 KMEEATAVSSEQNPVILIAVAVAGTIIIVFWFGFIIGRRHCGYSKADQEGDELYFHS 600
    |||
DB 541 KMEEATAVSSEQNPVILIAVAVAGTIIIVFWFGFIIGRRHCGYSKADQEGDELYFHS 600
QY 601 LYERGDGMKETOHNKKMMIASCSRL 626
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DB 601 LYERGDGMKETOHNKKMMIASCSRL 626
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RESULT 2

PCT-US96-00419-5
Sequence 5, Application PC/TUS9600419
GENERAL INFORMATION:
APPLICANT: Thomas Ciosesek, Axel Ulrich, Birgit
APPLICANT: Millauer
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: MDKI SIGNAL TRANSDUCTION DISORDERS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00419
FILING DATE: January 3, 1995
CLASSIFICATION:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: none
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 626
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-00419-5

Query Match 100.0%; Score 3338; DB 5; Length 626;
Best Local Similarity 100.0%; Pred. No. 1.3e-298;
Matches 626; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MVTQTRFSPSWIIICYYIMLGFPAHTGEAQAKEYLLDSKAQTELEWISSPPSGMEISG 60
    |||
DB 1 MVTQTRFSPSWIIICYYIMLGFPAHTGEAQAKEYLLDSKAQTELEWISSPPSGMEISG 60
QY 61 LDENYPIRTYQYQCVMEPNQNNWLRTNWSKGNARIFVELKFTLSDCNSLPGVLTGCK 120
    |||
DB 61 LDENYPIRTYQYQCVMEPNQNNWLRTNWSKGNARIFVELKFTLSDCNSLPGVLTGCK 120
QY 121 EFTENLYYEETDYDTGNIRRENLYVKIDTIADESFTQDGLGERKMKLNTVEIRIGPLSKK 180
    |||
DB 121 EFTENLYYEETDYDTGNIRRENLYVKIDTIADESFTQDGLGERKMKLNTVEIRIGPLSKK 180
QY 181 GFYLAFOVDGACIALVSVKYKKKWTIVENLAVFPDVTGSEFSSLVEVRGTCVSSAEE 240
    |||
DB 181 GFYLAFOVDGACIALVSVKYKKKWTIVENLAVFPDVTGSEFSSLVEVRGTCVSSAEE 240
QY 241 EAENSPPRMCSAAGEMLVPIGKICIKAGYQOKGDTCEPCGRRRYKSSSDLOCSRCPHIS 300
    |||
DB 241 EAENSPPRMCSAAGEMLVPIGKICIKAGYQOKGDTCEPCGRRRYKSSSDLOCSRCPHIS 300
QY 301 FSDREGSSRCECEDGYRRAPSDPPYACTRPPSAPQNLFININQTTVLSLWSPADNGR 360
    |||
DB 301 FSDREGSSRCECEDGYRRAPSDPPYACTRPPSAPQNLFININQTTVLSLWSPADNGR 360
QY 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQOTGLENDYVTWDLAAHANYFEVEAVNG 420
    |||
DB 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQOTGLENDYVTWDLAAHANYFEVEAVNG 420
QY 421 VSDLSRQRLFAAVSTTGAAPSQVSGWKERYLQRSVOLSQOEPHEHPGVITTEYIKY 480
    |||
DB 421 VSDLSRQRLFAAVSTTGAAPSQVSGWKERYLQRSVOLSQOEPHEHPGVITTEYIKY 480
QY 481 YEKDQERRTYTLTKTSTASINNLKPGTYVFOIRAVTAAGYNSPRLDVAITLLEASG 540
    |||
DB 481 YEKDQERRTYTLTKTSTASINNLKPGTYVFOIRAVTAAGYNSPRLDVAITLLEASG 540
QY 541 KMEEATAVSSEQNPVILIAVAVAGTIIIVFWFGFIIGRRHCGYSKADQEGDELYFHS 600
    |||
DB 541 KMEEATAVSSEQNPVILIAVAVAGTIIIVFWFGFIIGRRHCGYSKADQEGDELYFHS 600
QY 601 LYERGDGMKETOHNKKMMIASCSRL 626
    |||
DB 601 LYERGDGMKETOHNKKMMIASCSRL 626
```

RESULT 3

US-08-368-776A-3

Sequence 3, Application US/08368776A

Patent No. 6300482

GENERAL INFORMATION:

APPLICANT: Cioseck, Thomas

APPLICANT: Ullrich, Axel

APPLICANT: Millaet, Birgit

TITLE OF INVENTION: METHODS FOR DIAGNOSIS

TITLE OF INVENTION: AND TREATMENT OF MDK1

TITLE OF INVENTION: SIGNAL TRANSDUCTION

TITLE OF INVENTION: DISORDERS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: Storage

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08368, 776A

FILING DATE: January 3, 1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including application

APPLICATION NUMBER: described below: none

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 208/007

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 610 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-368-776A-3

Query Match 95.8%; Score 3199; DB 3; Length 610;
Best Local Similarity 100.0%; Pred. No. 7.8e-286;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVOOTRFPSWIIICITWILGFAHTEGAQAQAEVLLDLSKAQOTELWISSPPSGWEELSG 60
DB 1 MVOOTRFPSWIIICITWILGFAHTEGAQAQAEVLLDLSKAQOTELWISSPPSGWEELSG 60
QY 61 LDENVTPRTYQVCVMEPNQNNWLRITWISKNAQRIFFELKFTLRDQNSLPGLGTCK 120
DB 61 LDENVTPRTYQVCVMEPNQNNWLRITWISKNAQRIFFELKFTLRDQNSLPGLGTCK 120
QY 121 ETPNLYVETDYPGRNIRENLYVYKIDITIADESTOGDLGRKKKLTVEVREIGPLSKX 180
DB 121 ETPNLYVETDYPGRNIRENLYVYKIDITIADESTOGDLGRKKKLTVEVREIGPLSKX 180
QY 181 GFYLAFOVGACIALVSVKYYKKCWTIVENLAVPDTVTGSEFSLVEVGTCVSSAEE 240
DB 181 GFYLAFOVGACIALVSVKYYKKCWTIVENLAVPDTVTGSEFSLVEVGTCVSSAEE 240

DB 181 GFYLAFOVGACIALVSVKYYKKCWTIVENLAVPDTVTGSEFSLVEVGTCVSSAEE 240
QY 241 EAENSPRMHCSABEGEMLVPIGKCI CKAGYQOKGDTCEPCGRPFYKSSODLQCSRCPTHS 300
DB 241 EAENSPRMHCSABEGEMLVPIGKCI CKAGYQOKGDTCEPCGRPFYKSSODLQCSRCPTHS 300
QY 301 FSDREGSSRCECEGDYVRASDPYVACTRPPSPQNLININQTVLSLEWSPPADNGR 360
DB 301 FSDREGSSRCECEGDYVRASDPYVACTRPPSPQNLININQTVLSLEWSPPADNGR 360
QY 361 NDVTYRILCRCSWEQECPCGSSNIGYMPQOGLBNYTTWMDLAAHYTFEVEVANG 420
DB 361 NDVTYRILCRCSWEQECPCGSSNIGYMPQOGLBNYTTWMDLAAHYTFEVEVANG 420
QY 421 VSDLSRSQRLFAVSIITGQAAPSQVGVKERYLQSRVOLSMQEPHPNGVTEYEIKY 480
DB 421 VSDLSRSQRLFAVSIITGQAAPSQVGVKERYLQSRVOLSMQEPHPNGVTEYEIKY 480
QY 481 YEKDQERTYSTLTKTSTASINNLKPGYVFOIRA VTAAGYGNYSPLDVA TLLEASG 540
DB 481 YEKDQERTYSTLTKTSTASINNLKPGYVFOIRA VTAAGYGNYSPLDVA TLLEASG 540
QY 541 KMFPAIVSSBQNPVILIAVAVAGTILVPMYFGFIIGRRHCGYSKADQGBELYFHS 600
DB 541 KMFPAIVSSBQNPVILIAVAVAGTILVPMYFGFIIGRRHCGYSKADQGBELYFHS 600
QY 601 L 601
DB 601 L 601

RESULT 4

PCT-US96-00419-3

Sequence 3, Application PC/TUS9600419

GENERAL INFORMATION:

APPLICANT: Thomas Cioseck, Axel Ullrich, Birgit

APPLICANT: Millaet

TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF

TITLE OF INVENTION: MDK1 SIGNAL TRANSDUCTION DISORDERS

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM compatible

OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)

SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/00419

FILING DATE: January 3, 1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including application

APPLICATION NUMBER: described below: none

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 208/007

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 610

TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-00419-3

Query Match 95.8%; Score 3199; DB 5; Length 610;
Best Local Similarity 100.0%; Pred. No. 7.8e-286;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTQTRPSPMIIICYLWLGFAHTGEAQAKEVLLDLSKAQOTLEWISSPPSGMEISG 60
DB 1 MVTQTRPSPMIIICYLWLGFAHTGEAQAKEVLLDLSKAQOTLEWISSPPSGMEISG 60
QY 61 LBNYTPIRTYOVCQWMEPNQNNMLRTNWSKGAQRIFVELKFTLRDCLSLPGVIGTCK 120
DB 61 LBNYTPIRTYOVCQWMEPNQNNMLRTNWSKGAQRIFVELKFTLRDCLSLPGVIGTCK 120
QY 121 EFTNLYYYETDYGDNIRRENLVYKIDTIADESFTQDGLGERKMKLNTVEIREIGLSKK 180
DB 121 EFTNLYYYETDYGDNIRRENLVYKIDTIADESFTQDGLGERKMKLNTVEIREIGLSKK 180
QY 181 GFYLAFOVDGACIALVSVKYYKKCWITVENLAVFPDVTGSEFSSLVEVRGTCVSSAAE 240
DB 181 GFYLAFOVDGACIALVSVKYYKKCWITVENLAVFPDVTGSEFSSLVEVRGTCVSSAAE 240
QY 241 EAENSPPMHCSAEGEWLVPIGKCI CKAGYQOKGDTCEPCGRPFYKSSODLQCSRCPTHS 300
DB 241 EAENSPPMHCSAEGEWLVPIGKCI CKAGYQOKGDTCEPCGRPFYKSSODLQCSRCPTHS 300
QY 301 FSDRESSRCECEGYYRAPSDPPYVACTRPPSPQNLFININQTVTSLWSPADNGR 360
DB 301 FSDRESSRCECEGYYRAPSDPPYVACTRPPSPQNLFININQTVTSLWSPADNGR 360
QY 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQOTGLENDYVYMDLAAHYTFEVAVNG 420
DB 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQOTGLENDYVYMDLAAHYTFEVAVNG 420
QY 421 VSDLSRQRLFAVSIITGQAAPSOVSGWMEKERVLRQSVOLSWOEPHNGVITEYEIKY 480
DB 421 VSDLSRQRLFAVSIITGQAAPSOVSGWMEKERVLRQSVOLSWOEPHNGVITEYEIKY 480
QY 481 YEKDQERTYSTLTKTSTASINNLKPGTVVFOIRAVTAAGYGNVSPRLDVAITLEASG 540
DB 481 YEKDQERTYSTLTKTSTASINNLKPGTVVFOIRAVTAAGYGNVSPRLDVAITLEASG 540
QY 541 KMEEATVSSSEQNPVILIAVAVAGTILVFMVGFIIGRHCGYSKADGEBELYFHS 600
DB 541 KMEEATVSSSEQNPVILIAVAVAGTILVFMVGFIIGRHCGYSKADGEBELYFHS 600
QY 601 L 601
DB 601 L 601

RESULT 5
US-08-368-776A-12
Sequence 12, Application US/08368776A
Patent No. 6300482

GENERAL INFORMATION:
APPLICANT: Ciosek, Thomas
APPLICANT: Ulrich, Axel
TITLE OF INVENTION: METHODS FOR DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF MDK1
TITLE OF INVENTION: SIGNAL TRANSDUCTION
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California

COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/368,776A
FILING DATE: January 3, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 994 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-368-776A-12

Query Match 95.6%; Score 3191.5; DB 3; Length 994;
Best Local Similarity 95.9%; Pred. No. 8.3e-285;
Matches 605; Conservative 6; Mismatches 15; Indels 5; Gaps 2;

QY 1 MVTQTRPSPMIIICYLWLGFAHTGEAQAKEVLLDLSKAQOTLEWISSPPSGMEISG 60
DB 1 MVTQTRPSPMIIICYLWLGFAHTGEAQAKEVLLDLSKAQOTLEWISSPPSGMEISG 60
QY 61 LBNYTPIRTYOVCQWMEPNQNNMLRTNWSKGAQRIFVELKFTLRDCLSLPGVIGTCK 120
DB 61 LBNYTPIRTYOVCQWMEPNQNNMLRTNWSKGAQRIFVELKFTLRDCLSLPGVIGTCK 120
QY 121 EFTNLYYYETDYGDNIRRENLVYKIDTIADESFTQDGLGERKMKLNTVEIREIGLSKK 180
DB 121 EFTNLYYYETDYGDNIRRENLVYKIDTIADESFTQDGLGERKMKLNTVEIREIGLSKK 180
QY 181 GFYLAFOVDGACIALVSVKYYKKCWITVENLAVFPDVTGSEFSSLVEVRGTCVSSAAE 240
DB 181 GFYLAFOVDGACIALVSVKYYKKCWITVENLAVFPDVTGSEFSSLVEVRGTCVSSAAE 240
QY 241 EAENSPPMHCSAEGEWLVPIGKCI CKAGYQOKGDTCEPCGRPFYKSSODLQCSRCPTHS 300
DB 241 EAENSPPMHCSAEGEWLVPIGKCI CKAGYQOKGDTCEPCGRPFYKSSODLQCSRCPTHS 300
QY 301 FSDRESSRCECEGYYRAPSDPPYVACTRPPSPQNLFININQTVTSLWSPADNGR 360
DB 301 FSDRESSRCECEGYYRAPSDPPYVACTRPPSPQNLFININQTVTSLWSPADNGR 360
QY 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQOTGLENDYVYMDLAAHYTFEVAVNG 420
DB 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQOTGLENDYVYMDLAAHYTFEVAVNG 420
QY 421 VSDLSRQRLFAVSIITGQAAPSOVSGWMEKERVLRQSVOLSWOEPHNGVITEYEIKY 480
DB 421 VSDLSRQRLFAVSIITGQAAPSOVSGWMEKERVLRQSVOLSWOEPHNGVITEYEIKY 480
QY 481 YEKDQERTYSTLTKTSTASINNLKPGTVVFOIRAVTAAGYGNVSPRLDVAITLEASG 540
DB 481 YEKDQERTYSTLTKTSTASINNLKPGTVVFOIRAVTAAGYGNVSPRLDVAITLEASG 540

Qy 541 KMFATAVSSQONPVIIIAVAVAGTIIIVMVFGLIIRRHCGYSKADQSGDEELYFH 600
Db 541 KMFATAVSSQONPVIIIAVAVAGTIIIVMVFGLIIRRHCGYSKADQSGDEELYFH 600
Qy 601 ----LYRERGGMETQJN-KKMIASCSRL 626
Db 601 TKTYIDPETYEDPNRAVHQFAKELDASCIRI 631

RESULT 6

US-08-368-776A-2
; Sequence 2, Application US/08368776A
; Patent No. 6300482
; GENERAL INFORMATION:
; APPLICANT: Cioseck, Thomas
; APPLICANT: Ullrich, Axel
; APPLICANT: Millaer, Birgit
; TITLE OF INVENTION: METHODS FOR DIAGNOSIS
; TITLE OF INVENTION: AND TREATMENT OF MDK1
; TITLE OF INVENTION: SIGNAL TRANSDUCTION
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/368, 776A
; FILING DATE: January 3, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: none
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 998 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-368-776A-2

Query Match 95.6%; Score 3191; DB 3; Length 998;

Best Local Similarity 100.0%; Pred. No. 9.3e-285; Indels 0; Gaps 0;

Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVVOTRPPSWIILCYIMLGFAGTGEAQAQAEVLLDLSKAQOTELWISSPPSGMEETISG 60
Db 1 MVVOTRPPSWIILCYIMLGFAGTGEAQAQAEVLLDLSKAQOTELWISSPPSGMEETISG 60
Qy 61 LDENVYPIRTYQVCVMEPNQNNLRTNWSKNAQRIFWELKFTLDDCNLSPEVLGTCK 120
Db 61 LDENVYPIRTYQVCVMEPNQNNLRTNWSKNAQRIFWELKFTLDDCNLSPEVLGTCK 120

Db 61 LDENVYPIRTYQVCVMEPNQNNLRTNWSKNAQRIFWELKFTLDDCNLSPEVLGTCK 120
Qy 121 ETFNLYYEYEDDYDGRNIRENLVYKIDITIADESFOTGDGERKMLNTEVREIGPLSK 180
Db 121 ETFNLYYEYEDDYDGRNIRENLVYKIDITIADESFOTGDGERKMLNTEVREIGPLSK 180
Qy 181 GFYLAPODVAGACIALVSVKYYKKCWITVENLAVPDTVTGSEFSSLVEVRGTCVSSAEE 240
Db 181 GFYLAPODVAGACIALVSVKYYKKCWITVENLAVPDTVTGSEFSSLVEVRGTCVSSAEE 240
Qy 241 EAENSPPMHCSABEEMLVPIGKICIKAGYQOKGTCPCRCGRFRFKSSSODIQSCRCPTH 300
Db 241 EAENSPPMHCSABEEMLVPIGKICIKAGYQOKGTCPCRCGRFRFKSSSODIQSCRCPTH 300
Qy 301 FSDREGSSRCECEGYYRAPSDPPYVACTPPSPAPQULFININQTTLSLEMSPPADNGR 360
Db 301 FSDREGSSRCECEGYYRAPSDPPYVACTPPSPAPQULFININQTTLSLEMSPPADNGR 360
Qy 361 NDVTYRILCKRCSWEGECVPCGSGNIGYMPQQTGLEDDNYVTVDLAAHANYTFEVAVG 420
Db 361 NDVTYRILCKRCSWEGECVPCGSGNIGYMPQQTGLEDDNYVTVDLAAHANYTFEVAVG 420
Qy 421 VSDLSRQRLFAANSITTGQAAPQVSGMKERVLQRSVQLSWQEPHPNGVITEYEIKY 480
Db 421 VSDLSRQRLFAANSITTGQAAPQVSGMKERVLQRSVQLSWQEPHPNGVITEYEIKY 480
Qy 481 YEKQRERTYSLTKTSKTSASINNLKPGTYVFOIRAVTAAGYGNYSPPRLDVATLEBASG 540
Db 481 YEKQRERTYSLTKTSKTSASINNLKPGTYVFOIRAVTAAGYGNYSPPRLDVATLEBASG 540
Qy 541 KMFATAVSSQONPVIIIAVAVAGTIIIVMVFGLIIRRHCGYSKADQSGDEELYFH 599
Db 541 KMFATAVSSQONPVIIIAVAVAGTIIIVMVFGLIIRRHCGYSKADQSGDEELYFH 599

RESULT 7

PCT-US96-00419-2
; Sequence 2, Application PC/TUS9600419
; GENERAL INFORMATION:
; APPLICANT: Thomas Cioseck, Axel Ullrich, Birgit
; APPLICANT: Millaer
; TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: MDK1 SIGNAL TRANSDUCTION DISORDERS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00419
; FILING DATE: January 3, 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below: none
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 998
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; PCT: US96-00419-2

Query Match 95.6%; Score 3191; DB 5; Length 998;
 Best Local Similarity 100.0%; Pred. No. 9.3e-285;
 Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVVQTRPSPWIIICYYIMLGFATGGAQAQAEVLLDLSKAQOETELEMISPPSGMEISG 60
 DB 1 MVVQTRPSPWIIICYYIMLGFATGGAQAQAEVLLDLSKAQOETELEMISPPSGMEISG 60
 QY 61 LDENYTPIRTYQVCQVMEPNQNNMLRTNWSKGAQRIFVELKFTLRDCNSLPGLGTCK 120
 DB 61 LDENYTPIRTYQVCQVMEPNQNNMLRTNWSKGAQRIFVELKFTLRDCNSLPGLGTCK 120
 QY 121 ETENLYYETDYGIRNIRENLVYKIDTIAADESFTQDGERKMKLNTREIIGPLSKK 180
 DB 121 ETENLYYETDYGIRNIRENLVYKIDTIAADESFTQDGERKMKLNTREIIGPLSKK 180
 QY 181 GFYLAPODVACIALYVSVKYYKKCWTIYENLAVFPDVTGSEFSSLVEVRGTCVSSAAE 240
 DB 181 GFYLAPODVACIALYVSVKYYKKCWTIYENLAVFPDVTGSEFSSLVEVRGTCVSSAAE 240
 QY 241 EAENSPPMHCSABGEMLVPIGKCI CKAGYQOKGDTCEPCGRFRYKSSODLQCSRCPTHS 300
 DB 241 EAENSPPMHCSABGEMLVPIGKCI CKAGYQOKGDTCEPCGRFRYKSSODLQCSRCPTHS 300
 QY 301 FSDREGSSRCCEGDYTRAPSDPPYVACTRPPAPQNLIFNINQTVLSLEWSPADNGGR 360
 DB 301 FSDREGSSRCCEGDYTRAPSDPPYVACTRPPAPQNLIFNINQTVLSLEWSPADNGGR 360
 QY 361 NDVTYRILCKRCSEGECEVPCGSNIGYMPQOGLGLEDNYTVVMDLAAHANYTPEVAANG 420
 DB 361 NDVTYRILCKRCSEGECEVPCGSNIGYMPQOGLGLEDNYTVVMDLAAHANYTPEVAANG 420
 QY 421 VSDLSRQRLFAAVSITTTGQAAPQVSGVWKERVLDORSVOLSWQEPHEHPGVITEYIKY 480
 DB 421 VSDLSRQRLFAAVSITTTGQAAPQVSGVWKERVLDORSVOLSWQEPHEHPGVITEYIKY 480
 QY 481 YEKDQERTYSTLTKTSTASINNLKPGTYVFOIRAVTAAGYGNYSPLDVAATLEBASG 540
 DB 481 YEKDQERTYSTLTKTSTASINNLKPGTYVFOIRAVTAAGYGNYSPLDVAATLEBASG 540
 QY 541 KMFETAVSSBQNVIIIAVAVAGTIIIVFMVFGFIIGRRHCGYSADQGBDELAEPH 599
 DB 541 KMFETAVSSBQNVIIIAVAVAGTIIIVFMVFGFIIGRRHCGYSADQGBDELAEPH 599

RESULT 8
 US-08-368-776A-11
 ; Sequence 11, Application US/08368776A
 ; Patent No. 6300482

; GENERAL INFORMATION:
 ; APPLICANT: Cissek, Thomas
 ; APPLICANT: Ulirich, Axel
 ; APPLICANT: Milauer, Birgit
 ; TITLE OF INVENTION: METHODS FOR DIAGNOSIS
 ; TITLE OF INVENTION: AND TREATMENT OF MDK1
 ; TITLE OF INVENTION: SIGNAL TRANSDUCTION
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California

; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: Storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/368,776A
 ; FILING DATE: January 3, 1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; PRIOR APPLICATION DATA: including application
 ; PRIOR APPLICATION DATA: described below: none
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 208/007
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 993 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-368-776A-11

Query Match 94.4%; Score 3151.5; DB 3; Length 993;
 Best Local Similarity 99.2%; Pred. No. 4e-281; Indels 5; Gaps 1;
 Matches 594; Conservative 0; Mismatches 0;

QY 1 MVVQTRPSPWIIICYYIMLGFATGGAQAQAEVLLDLSKAQOETELEMISPPSGMEISG 60
 DB 1 MVVQTRPSPWIIICYYIMLGFATGGAQAQAEVLLDLSKAQOETELEMISPPSGMEISG 60
 QY 61 LDENYTPIRTYQVCQVMEPNQNNMLRTNWSKGAQRIFVELKFTLRDCNSLPGLGTCK 120
 DB 61 LDENYTPIRTYQVCQVMEPNQNNMLRTNWSKGAQRIFVELKFTLRDCNSLPGLGTCK 120
 QY 121 ETENLYYETDYGIRNIRENLVYKIDTIAADESFTQDGERKMKLNTREIIGPLSKK 180
 DB 121 ETENLYYETDYGIRNIRENLVYKIDTIAADESFTQDGERKMKLNTREIIGPLSKK 180
 QY 181 GFYLAPODVACIALYVSVKYYKKCWTIYENLAVFPDVTGSEFSSLVEVRGTCVSSAAE 240
 DB 181 GFYLAPODVACIALYVSVKYYKKCWTIYENLAVFPDVTGSEFSSLVEVRGTCVSSAAE 240
 QY 241 EAENSPPMHCSABGEMLVPIGKCI CKAGYQOKGDTCEPCGRFRYKSSODLQCSRCPTHS 300
 DB 241 EAENSPPMHCSABGEMLVPIGKCI CKAGYQOKGDTCEPCGRFRYKSSODLQCSRCPTHS 300
 QY 301 FSDREGSSRCCEGDYTRAPSDPPYVACTRPPAPQNLIFNINQTVLSLEWSPADNGGR 360
 DB 301 FSDREGSSRCCEGDYTRAPSDPPYVACTRPPAPQNLIFNINQTVLSLEWSPADNGGR 360
 QY 361 NDVTYRILCKRCSEGECEVPCGSNIGYMPQOGLGLEDNYTVVMDLAAHANYTPEVAANG 420
 DB 361 NDVTYRILCKRCSEGECEVPCGSNIGYMPQOGLGLEDNYTVVMDLAAHANYTPEVAANG 420
 QY 421 VSDLSRQRLFAAVSITTTGQAAPQVSGVWKERVLDORSVOLSWQEPHEHPGVITEYIKY 480
 DB 421 VSDLSRQRLFAAVSITTTGQAAPQVSGVWKERVLDORSVOLSWQEPHEHPGVITEYIKY 480
 QY 481 YEKDQERTYSTLTKTSTASINNLKPGTYVFOIRAVTAAGYGNYSPLDVAATLEBASG 540
 DB 481 YEKDQERTYSTLTKTSTASINNLKPGTYVFOIRAVTAAGYGNYSPLDVAATLEBASG 540

QY 541 KMFEATAVSSSEONPVIIIAVAVAGTIIIVFVFGFIIIGRRHCGSKADQEGDEELYPH 599
DB 540 ----ATAVSSSEONPVIIIAVAVAGTIIIVFVFGFIIIGRRHCGSKADQEGDEELYPH 594

RESULT 9
US-08-449-645A-17

Sequence 17, Application US/08449645A

Patent No. 5981245

GENERAL INFORMATION:

APPLICANT: Fox, Gary M.

TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine

TITLE OF INVENTION: Kinases

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Patent Operations/RBW

STREET: 1840 Dehavilland Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/449,645A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Winter, Robert B.

REFERENCE/DOCKET NUMBER: A-287

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 998 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-449-645A-17

Query Match 94.0%; Score 3139; DB 2; Length 998;

Best Local Similarity 97.7%; Pred. No. 5.8e-280;

Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

QY 1 MVQTRPSPSWIILCYIWLGFHAGTGEAQAKEVLLDSKAQOTLEWISSPPSGWEIISG 60
DB 1 MVQTRPSPSWIILCYIWLGFHAGTGEAQAKEVLLDSKAQOTLEWISSPPSGWEIISG 60
QY 61 LDENTPTIRTYOVQVMEPNQNNMLRTNWSKGNQRIFFVELKFTLRDQNSLPVLTGTC 120
DB 61 LDENTPTIRTYOVQVMEPNQNNMLRTNWSKGNQRIFFVELKFTLRDQNSLPVLTGTC 120
QY 121 EFTNLYYETDYDGRNIRENLYVKIDITIADESFTOGDLGERKKKLTVEVREIPLSK 180
DB 121 EFTNLYYETDYDGRNIRENLYVKIDITIADESFTOGDLGERKKKLTVEVREIPLSK 180
QY 181 GFYLAFOVGACIALVSVKYYKKCWTIVENLAVPDTVTGSEFSSLVEVRGTCVSSAE 240
DB 181 GFYLAFOVGACIALVSVKYYKKCWTIVENLAVPDTVTGSEFSSLVEVRGTCVSSAE 240
QY 241 EAENSPRMHCSAEGEWLPVIGKCIKAGYQOKGDTCEPCGRFPYKSSQDLQCSRCPHS 300
DB 241 EAENSPRMHCSAEGEWLPVIGKCIKAGYQOKGDTCEPCGRFPYKSSQDLQCSRCPHS 300
QY 301 FSDRSGSSRCECEDGYRAPSDPPYVACTRPSPAPONLIFNINQTTVSLSESPPADNGR 360
DB 301 FSDRSGSSRCECEDGYRAPSDPPYVACTRPSPAPONLIFNINQTTVSLSESPPADNGR 360
QY 361 NDVTYRIILCKRCMSWQEGECVPCGSGNIGYMPQOTGLEEDNYVTVMDLIAHANYTFEYEA 420
DB 361 NDVTYRIILCKRCMSWQEGECVPCGSGNIGYMPQOTGLEEDNYVTVMDLIAHANYTFEYEA 420

QY 421 VSDLSRSQRLFAAVSITTGQAAPSOVSGWMEKRVLOREVOJSMOPEHPNGVITEYIKY 480
DB 421 VSDLSRSQRLFAAVSITTGQAAPSOVSGWMEKRVLOREVOJSMOPEHPNGVITEYIKY 480

QY 481 YEKDQERTYSTLTKTSASINNLKPGTYVYFQIRAVTAAGYGNYSRDLVATLEASG 540
DB 481 YEKDQERTYSTLTKTSASINNLKPGTYVYFQIRAVTAAGYGNYSRDLVATLEASG 540

QY 541 KMFEATAVSSSEONPVIIIAVAVAGTIIIVFVFGFIIIGRRHCGSKADQEGDEELYPH 599
DB 541 KMFEATAVSSSEONPVIIIAVAVAGTIIIVFVFGFIIIGRRHCGSKADQEGDEELYPH 599

RESULT 10
US-08-702-367A-17

Sequence 17, Application US/08702367A

Patent No. 5981246

GENERAL INFORMATION:

APPLICANT: Fox, Gary M.

TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine

TITLE OF INVENTION: Kinases

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Patent Operations/RBW

STREET: 1840 Dehavilland Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: USA

ZIP: 91320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/702,367A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Winter, Robert B.

REFERENCE/DOCKET NUMBER: A-287

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 998 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-702-367A-17

Query Match 94.0%; Score 3139; DB 2; Length 998;

Best Local Similarity 97.7%; Pred. No. 5.8e-280;

Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

QY 1 MVQTRPSPSWIILCYIWLGFHAGTGEAQAKEVLLDSKAQOTLEWISSPPSGWEIISG 60
DB 1 MVQTRPSPSWIILCYIWLGFHAGTGEAQAKEVLLDSKAQOTLEWISSPPSGWEIISG 60
QY 61 LDENTPTIRTYOVQVMEPNQNNMLRTNWSKGNQRIFFVELKFTLRDQNSLPVLTGTC 120
DB 61 LDENTPTIRTYOVQVMEPNQNNMLRTNWSKGNQRIFFVELKFTLRDQNSLPVLTGTC 120
QY 121 EFTNLYYETDYDGRNIRENLYVKIDITIADESFTOGDLGERKKKLTVEVREIPLSK 180
DB 121 EFTNLYYETDYDGRNIRENLYVKIDITIADESFTOGDLGERKKKLTVEVREIPLSK 180
QY 181 GFYLAFOVGACIALVSVKYYKKCWTIVENLAVPDTVTGSEFSSLVEVRGTCVSSAE 240
DB 181 GFYLAFOVGACIALVSVKYYKKCWTIVENLAVPDTVTGSEFSSLVEVRGTCVSSAE 240
QY 241 EAENSPRMHCSAEGEWLPVIGKCIKAGYQOKGDTCEPCGRFPYKSSQDLQCSRCPHS 300
DB 241 EAENSPRMHCSAEGEWLPVIGKCIKAGYQOKGDTCEPCGRFPYKSSQDLQCSRCPHS 300

| | | | | | |
|----|-----|----------------------|---------------------|---------------------|-----|
| QY | 301 | PSDRGSSKSCBCEDDGYRPA | SPDPBPYACRPSAPQNL | FNINQTVSLSPNSPANGGR | 360 |
| Db | 301 | PSDKGSSKSCBCEDDGYRPA | SDPBPYACRPSAPQNL | FNINQTVSLSPNSPADNGR | 360 |
| QY | 361 | NDVTRILCKRCSWEGECVPC | SGSNGYMPQOTGLDENVTY | VMDLAAHANFTFEVEAVNG | 420 |
| Db | 361 | NDVTRILCKRCSWEGECVPC | SGSNGYMPQOTGLDENVTY | VMDLAAHANFTFEVEAVNG | 420 |
| QY | 421 | VSDLSRSQLPFAAVSTTTGO | APSPQYSGMKKEVILQRSV | OLSMQEBHPH3VTTXEIKY | 480 |
| Db | 421 | VSDLSRSQLPFAAVSTTTGO | APSPQYSGMKKEVILQRSV | OLSMQEBHPH3VTTXEIKY | 480 |
| QY | 481 | YEKQORERTYSTLTKTST | SASINNLKPGTYVYFQIR | AVAAAGYGNYSPLJVA | 540 |
| Db | 481 | YEKQORERTYSTLTKTST | SASINNLKPGTYVYFQIR | AVAAAGYGNYSPLJVA | 540 |
| QY | 541 | KMEFEATVASSEQNPVIL | ILVVAAGTILIVPMVFG | RTIGRRHCGSKAAQSG | 600 |
| Db | 541 | KMEFEATVASSEQNPVIL | ILVVAAGTILIVPMVFG | RTIGRRHCGSKAAQSG | 600 |

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RESULT 11
US-09-949-016-6501
; Sequence 6501, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 6501
; LENGTH: 998
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6501

Query Match          94.0%; Score 3139; DB 4; Length 998;
Best Local Similarity 97.7%; Pred. No. 5,8e-280;
Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

1  MVVQTRFPEWIIILCYIWLIGFAHTGEAQAKEYLLDLSKAQOOTELEWIS:PPSGMEIRSG 60
Db 1  MVQTRFPEWIIILCYIWLIRFAHTGEAQAKEYLLDLSKAQOOTELEWIS:PPNGMEIRSG 60
OY 61  IDENTYPIRTYQVCQVMEPNQNNWMLRTNMISKNAQRIFVELKFTLRDCHSLPGVIGTCK 120
Db 61  IDENTYPIRTYQVCQVMEPNQNNWMLRTNMISKNAQRIFELKFTLRDCHSLPGVIGTCK 120
OY 121  EFTFNLYYYTDDVDGTGNIRENLVYKIDTIAADESFFQGDUGERKMKLNTIVREIGPLSK 180
Db 121  EFTFNLYYYTDDVDGTGNIRENLVYKIDTIAADESFFQGDUGERKMKLNTIVREIGPLSK 180
OY 181  GFLYLFQDVGACIALVSVKVYKCKMTIENLAVFPDPTLVGSSEFSLVVEVRGTVSSAAE 240
Db 181  GFLYLFQDVGACIALVSVKVYKCKMTIENLAVFPDPTLVGSSEFSLVVEVRGTVSSAAE 240
OY 241  EAENSPPRMKCSAEGEWLVPIGKCIICAKAGYQOKGDTEPCGGRFRYKSSQDILQSCRPTHS 300
Db 241  EAENNAPRMHCASBGEWLVPIGKCIICAKAGYQOKGDTEPCGGRFRYKSSQDILQSCRPTHS 300
OY 301  FSDRECSFCECEBDGYIRAPSDPPYIACTRPPSAPONLFFNIQTTVLSLWSPPADNGR 360
Db 301  FSDRECSFCECEBDGYIRAPSDPPYIACTRPPSAPONLFFNIQTTVLSLWSPPADNGR 360

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| | | | |
|----|-----|---|-----|
| Db | 301 | FSDKSGSSRCBCEBDGYAAPSDDPYVACTRPPSAQNLFINNQTTVLSLEWSPANDGR | 360 |
| Qy | 361 | NDVTYRIILCKRCSMQEGECVPCGSGNIGYMPQDTGEDNVTYVMDLIAHANYTFEVEAVNG | 420 |
| Db | 361 | NDVTYRIILCKRCSMQEGECVPCGSGNIGYMPQDTGEDNVTYVMDLIAHANYTFEVEAVNG | 420 |
| Qy | 421 | VSDLSRSQRLFAAASITTTGQAAPSOVSGVMKRVLQRSVLQSMQEBEHNGVTEYEIKY | 480 |
| Db | 421 | VSDLSRSQRLFAAASITTTGQAAPSOVSGVMKRVLQRSVELQSMQEBEHNGVTEYEIKY | 480 |
| Qy | 481 | YEKQDRERTYSTLTKTSTSSASINLNKPGTVVYFOJIRAVYAAGYGNYSPLDVAATLEASG | 540 |
| Db | 481 | YEKQDRERTYSTLTKTSTSSASINLNKPGTVVYFOJIRAFYAAGYGNYSPLDVAATLEASG | 540 |
| Qy | 541 | KMEFETAAVSSBEONPVIIIAVAVAVAGTIIIVFVWPGTIIIGRRHCGYSKAOEGDEELTYFH | 599 |
| Db | 541 | KMEFETAAVSSBEONPVIIIAVAVAVAGTIIIVFVWPGTIIIGRRHCGYSKAOEGDEELTYFH | 599 |

```

RESULT 12
PCT-US95-04681-17
/ Sequence 17, Application PC/TUS9504681
/ GENERAL INFORMATION:
/ APPLICANT: Fox, Gary M.
/ TITLE OF INVENTION: Eph-Like Receptor Protein Tyrosine
/ TITLE OF INVENTION: Kinases
/ NUMBER OF SEQUENCES: 28
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Amgen Patent Operations/RBW
/ STREET: 1840 Dehavilland Drive
/ CITY: Thousand Oaks
/ STATE: California
/ COUNTRY: USA
/ ZIP: 91320
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US95/04681
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Winteer, Robert B.
/ REFERENCE/DOCKET NUMBER: A-287
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 998 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ PCT-US95-04681-17

Query Match          94.0%; Score 3139; DB 5; Length 998;
Best Local Similarity 97.7%; Pred. No. 5.8e-280;
Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

1 M V V O T R F P S W I I L C Y I M L L G F A H T G E A O A K E V L L D S K A O Q T L E W I S S P P S G M E E I S G 60
1 M V F Q T R Y S W I I L C Y I M L L R P A H T G E A O A K E V L L D S K A O Q T L E W I S S P P N G M E E I S G 60
1 D E N V Y T P I R T O V O C W E P N O N M L R T N M I S K G N A O R I F V E L K F T L R D C N S L P G V L G T C K 120
61 I D E N V Y T P I R T O V O C W E P N O N M L R T N M I S K G N A O R I F V E L K F T L R D C N S L P G V L G T C K 120
121 E T F N L Y Y E T D Y D T G R N I R E N L Y Y K I D T I A D E S F T G D L G E R K M K L N T E V R E I G P L S K K 180
121 E T F N L Y Y E T D Y D T G R N I R E N L Y Y K I D T I A D E S F T G D L G E R K M K L N T E V R E I G P L S K K 180
181 G E Y L A F O V G A C I A L N S K V Y Y K K C W T I V E N L A V F P D T V G S E F S S I V E V R G C T V S S A E E 240
181 G E Y L A F O V G A C I A L N S K V Y Y K K C W S I I E N L A I F P D T V G S E F S S I V E V R G C T V S S A E E 240

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Db 128 NMVFESDDONGRNKIKENQYIKIDTIADESFTELDIDGRVMTKTEVRDZPLSKKGFY 187
QY 184 LAFODVACIALVSVKYYKKCWITVENLAVFPDVTGSEFSSLVEYRGTCVSAEBEAE 243
Db 188 LAFODVACIALVSVRYKKCPVNRHLAVFPDITIGADSSQLLEVSGSCVN--HSVTD 245
QY 244 NSPRMCSAEGEWLVPIGKCTCKAGYQOKGDTCEPCGRRFYKSSQDLQSCRPTHSFSD 303
Db 246 EPPRMCSAEGEWLVPIGKCMCKAGYEKNKGTCCVCRPGFFKASPHIQSCGKCPHSHYTH 305
QY 304 REGSSRCECEDGYRRAPSDPPYVACTRPPAPQNLFININOTVLSLEMSPPADNGGRNDV 363
Db 306 EEAISTCVCEKDYFRRESDPPTMACTRPSPAPRNALSNVNETSVFLEWLPADTGKRDV 365
QY 364 TYRILKRCSEWQECVPCGSNIGYMPQOTGLEBDNYTVMDLLAHANYTFEVEAVNGVSD 423
Db 366 SYIACKCKNSHAGVECECGHVRYLPRQSLKNTSVWMDLLAHNTYTFEIEAVNGVSD 425
QY 424 LSRSQLFAAVSITTGQAAPSOVSQVWKERYLQRSVQLSWQEPHNGVITEYEIKYYEK 483
Db 426 LSPGARQYVSVNVTNOAAPSPVTNVKKGKIAKNSISLSWQEPDRPNGIILEYEIKHFEK 485
QY 484 DQERTYSTLKTSTASINLKRGTYYVQIRAVTAAGVGNVSPRLDVATLEASGMF 543
Db 486 DQ-ETSTYITIKSKETITABGLKPASVYVFOIRARTAGYGVFSRFE-----F 533
QY 544 EAT---AVSSEQNPIIIVAVAGTIIIVFMVFGFIIGRRHCGYSKADQGDDE-LYFH 599
Db 534 ETTVPFAASDQSQIPVIASVTVG-VILLAVIGVLLSGRCGYSAKQDPBEKMHFH 592
QY 600 S 600
Db 593 N 593

RESULT 15
US-08-702-367A-13
; Sequence 13, Application US/08702367A
; Patent No. 5981246
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; TITLE OF INVENTION: Eph-like Receptor Protein Tyrosine
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Patent Operations/RM
; STREET: 1840 Denavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702,367A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-287
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 991 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-702-367A-13

Query Match 55.2%; Score 1841; DB 2; Length 991;
Best Local Similarity 57.4%; Pred. No. 2,5e-160;

Matches 345; Conservative 97; Mismatches 133; Indels 26; Gaps 8;
QY 6 RPSM--IILCYIMLGFATGEOAKAEVLLDSKAQOTELMISPPSGWEEISGLDE 63
Db 13 RAPLMTCILIC-----AALRTILASPSNEVNLDSRTWMDLQWIFPKKMGWEIGVDE 67
QY 64 NYPIRTYQCVQMEPNQNNMLRTNWSKGNARIVELKFTLRDQNSLPVGLTCKETP 123
Db 68 NYAPIHTYQCVKMEQNNMMLTWSISNEGAGRIFELFTLRDQNSLPGLGTCKETP 127
QY 124 NLVYERDVTGNTNIRBNLVKIDTIADESFTQDGLGEKMKLNTREIRIGPLSKKGFY 183
Db 128 NMVFESDDONGRNKIKENQYIKIDTIADESFTELDIDGRVMTKTEVRDZPLSKKGFY 187
QY 184 LAFODVACIALVSVKYYKKCWITVENLAVFPDVTGSEFSSLVEYRGTCVSAEBEAE 243
Db 188 LAFODVACIALVSVRYKKCPVNRHLAVFPDITIGADSSQLLEVSGSCVN--HSVTD 245
QY 244 NSPRMCSAEGEWLVPIGKCTCKAGYQOKGDTCEPCGRRFYKSSQDLQSCRPTHSFSD 303
Db 246 EPPRMCSAEGEWLVPIGKCMCKAGYEKNKGTCCVCRPGFFKASPHIQSCGKCPHSHYTH 305
QY 304 REGSSRCECEDGYRRAPSDPPYVACTRPPAPQNLFININOTVLSLEMSPPADNGGRNDV 363
Db 306 EEAISTCVCEKDYFRRESDPPTMACTRPSPAPRNALSNVNETSVFLEWLPADTGKRDV 365
QY 364 TYRILKRCSEWQECVPCGSNIGYMPQOTGLEBDNYTVMDLLAHANYTFEVEAVNGVSD 423
Db 366 SYIACKCKNSHAGVECECGHVRYLPRQSLKNTSVWMDLLAHNTYTFEIEAVNGVSD 425
QY 424 LSRSQLFAAVSITTGQAAPSOVSQVWKERYLQRSVQLSWQEPHNGVITEYEIKYYEK 483
Db 426 LSPGARQYVSVNVTNOAAPSPVTNVKKGKIAKNSISLSWQEPDRPNGIILEYEIKHFEK 485
QY 484 DQERTYSTLKTSTASINLKRGTYYVQIRAVTAAGVGNVSPRLDVATLEASGMF 543
Db 486 DQ-ETSTYITIKSKETITABGLKPASVYVFOIRARTAGYGVFSRFE-----F 533
QY 544 EAT---AVSSEQNPIIIVAVAGTIIIVFMVFGFIIGRRHCGYSKADQGDDE-LYFH 599
Db 534 ETTVPFAASDQSQIPVIASVTVG-VILLAVIGVLLSGRCGYSAKQDPBEKMHFH 592
QY 600 S 600
Db 593 N 593

Search completed: August 23, 2005, 08:27:36
Job time : 23.7783 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 23, 2005, 08:26:40 ; Search time 71.9191 Seconds
(without alignments)
3366.450 Million cell updates/sec

Title: US-10-073-064-5
Perfect score: 3338
Sequence: 1 MVVQTRPPRSIIICYLWLG.....DGMEKTOHKKMKIASCSRL 626

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | # Query Match | Length | ID | Description |
|------------|--------|---------------|--------|----|--------------------|
| 1 | 3338 | 100.0 | 626 | 2 | AAW03423 Mouse dev |
| 2 | 3199 | 95.8 | 610 | 2 | AAW03422 Mouse dev |
| 3 | 3191 | 95.6 | 998 | 2 | AAW03421 Mouse dev |
| 4 | 3139 | 94.0 | 945 | 8 | ADM87167 Human pro |
| 5 | 3139 | 94.0 | 998 | 2 | AAW85092 EPH-like |
| 6 | 1841 | 55.2 | 991 | 2 | AAW85092 EPH-like |
| 7 | 1830.5 | 54.8 | 953 | 5 | ABP52826 Human rec |
| 8 | 1822 | 54.6 | 1005 | 2 | AAW83147 Rat recep |
| 9 | 1822 | 54.6 | 1037 | 5 | ABR44241 Tyrosine |
| 10 | 1817 | 54.4 | 1037 | 5 | ABG61868 Prostate |
| 11 | 1817 | 54.4 | 1037 | 7 | ADG31683 Human 141 |
| 12 | 1806.5 | 54.1 | 975 | 5 | ABP52827 Human Etk |
| 13 | 1796 | 53.8 | 983 | 3 | AAW08665 Amino aci |
| 14 | 1796 | 53.8 | 983 | 3 | AAW08666 A human E |
| 15 | 1796 | 53.8 | 983 | 6 | ABR57491 Human Eph |
| 16 | 1796 | 53.8 | 983 | 7 | AAE38583 Human rec |
| 17 | 1796 | 53.8 | 983 | 7 | ADB75273 Prostate |
| 18 | 1796 | 53.8 | 983 | 7 | ADD48947 Human Pro |
| 19 | 1796 | 53.8 | 983 | 7 | ADN39284 Cancer/an |
| 20 | 1787.5 | 53.6 | 984 | 7 | ADD48945 Rat Prote |
| 21 | 1783.5 | 53.4 | 968 | 5 | ABP52825 Chicken r |
| 22 | 1775.5 | 53.2 | 983 | 2 | AAW75711 Eph-relat |
| 23 | 1770 | 53.0 | 983 | 2 | AAW31466 HEK polyp |
| 24 | 1741.5 | 52.2 | 833 | 7 | ADM29344 Human nov |
| 25 | 1741.5 | 52.2 | 921 | 5 | ABG79685 Tumour in |

| | | | | | |
|----|--------|------|------|---|--------------------|
| 26 | 1741.5 | 52.2 | 949 | 7 | ADM29342 Human nov |
| 27 | 1741.5 | 52.2 | 986 | 2 | AAW85091 EPH-like |
| 28 | 1741.5 | 52.2 | 986 | 7 | ADD46395 Human Pro |
| 29 | 1741.5 | 52.2 | 986 | 8 | ADQ17780 Human bof |
| 30 | 1741.5 | 52.2 | 986 | 8 | ADP54599 Human EPH |
| 31 | 1741.5 | 52.2 | 997 | 4 | ABG05689 Novel hum |
| 32 | 1741.5 | 52.2 | 1026 | 4 | ABG22931 Novel hum |
| 33 | 1737.5 | 52.1 | 539 | 3 | AAW08667 A human E |
| 34 | 1734.5 | 52.0 | 966 | 2 | AAW85936 Protein t |
| 35 | 1701.5 | 51.0 | 935 | 8 | ADP43499 Human eph |
| 36 | 1701.5 | 51.0 | 935 | 8 | ADJ88175 Human EPH |
| 37 | 1701.5 | 51.0 | 992 | 4 | AAW00691 Ephrin ty |
| 38 | 1701.5 | 51.0 | 992 | 5 | AAE23799 Ephrin ty |
| 39 | 1701.5 | 51.0 | 1005 | 5 | ABP69349 Human pol |
| 40 | 1701.5 | 51.0 | 1005 | 8 | ADP43465 Human eph |
| 41 | 1701.5 | 51.0 | 1005 | 8 | ADJ88141 Human EPH |
| 42 | 1701.5 | 51.0 | 1012 | 4 | AAE04362 Human kin |
| 43 | 1699.5 | 50.9 | 935 | 8 | ADP43497 Human eph |
| 44 | 1699.5 | 50.9 | 935 | 8 | ADJ88173 Human EPH |
| 45 | 1671 | 50.1 | 1035 | 5 | ABG70391 Human EPH |

ALIGNMENTS

| | | |
|----------|---|--|
| RESULT 1 | AAW03423 | standard; protein; 626 AA. |
| ID | AAW03423 | |
| XX | AAW03423; | |
| AC | | |
| DT | 11-NOV-1996 | (first entry) |
| XX | | |
| DE | Mouse developmental kinase 1 MDK1 T2. | |
| XX | | |
| KW | Mouse developmental kinase 1; MDK1 T2; receptor tyrosine kinase; RTK; | |
| KW | signal transduction; probe; diagnosis; gene therapy; neurodegeneration; | |
| KW | neuroproliferation; cancer. | |
| XX | | |
| OS | Mus sp. | |
| XX | | |
| FX | Key | Location/Qualifiers |
| FT | Peptide | 1..28 |
| FT | | /label= sig_peptide |
| FT | Modified-site | 64..66 |
| FT | | /label= N-glycosylation_site |
| FT | Modified-site | 343..345 |
| FT | | /label= N-glycosylation_site |
| FT | Modified-site | 410..412 |
| FT | | /label= N-glycosylation_site |
| FT | Domain | 555..579 |
| FT | | /label= Transmembrane_domain |
| FT | Misc-difference | 600..626 |
| FT | | /note= "product of alternative splicing" |
| PN | W09621013-A1. | |
| XX | | |
| PD | 11-JUL-1996. | |
| XX | | |
| PF | 03-JAN-1996; | 96WO-US000419. |
| XX | | |
| PR | 03-JAN-1995. | 95US-00368776. |
| XX | | |
| PA | (SUGEN-) SUGEN INC. | |
| PA | (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN. | |
| XX | | |
| PI | Closesek T, Ullrich A, Millaer B; | |
| XX | | |
| DR | WPI: 1996-333988/33. | |
| DR | N-PSDB; AAT32962. | |
| XX | | |
| PT | New mouse development kinase 1 gene - used for developing prods. for | |
| PT | diagnosis and treatment of abnormalities in signal transduction pathways. | |

XX Example 1; Page 113-115; 128bp; English.
XX
XX CDNA cloning using adult mouse brains and Northern blotting identified 2
XX truncated versions, MDK1 T1 (AAW03422) and MDK1 T2 (AAW03423), of the
XX novel mouse developmental kinase 1 (MDK1) (see also AAW03421), a new
XX member of the eck/eph family of receptor tyrosine kinases. Their amino
XX acid sequences were deduced from cDNA clones (AAT32961 and AAT32962)
XX obtd. from adult mouse brains. MDK T1 and T2 each possess the entire
XX ectodomain, the transmembrane domain and part of the juxtamembrane region
XX of MDK1, but lack the catalytic tyrosine kinase domain. They can be used
XX to screen for potential agents useful for treatment of diseases
XX characterised by abnormal signal transduction
XX

Sequence 626 AA:

Query Match 100.0%; Score 3338; DB 2; Length 625;
Best Local Similarity 100.0%; Pred. No. 1e-286; Mismatches 0; Indels 0; Gaps 0;
Matches 626; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTQTFPSPWIIICYIWLGFAGTGAQAQAEVLLDLSKAQOTELEWISSPSGWEISG 60
DB 1 MVTQTFPSPWIIICYIWLGFAGTGAQAQAEVLLDLSKAQOTELEWISSPSGWEISG 60
QY 61 LDENYPIRTYQVCQWEPNQNMLRTNWSKGNARIFVELKFTLRDQNSLPGVIGTCK 120
DB 61 LDENYPIRTYQVCQWEPNQNMLRTNWSKGNARIFVELKFTLRDQNSLPGVIGTCK 120
QY 121 EFTNLYYYETDYGIRNIRENLVYKIDITIADESFTQDGLGERKMKLNTVEIREIGPLSKK 180
DB 121 EFTNLYYYETDYGIRNIRENLVYKIDITIADESFTQDGLGERKMKLNTVEIREIGPLSKK 180
QY 181 GFYLAFOVDGACIALVSVKYYKKCWTIVENLAVFPDVTGSEFSSLVEVRGTCVSSAAE 240
DB 181 GFYLAFOVDGACIALVSVKYYKKCWTIVENLAVFPDVTGSEFSSLVEVRGTCVSSAAE 240
QY 241 EAENSPPRMHCSAGEWLVPIGKCI CKAQYQKGDTPCEGRRTYKSSSDLOCRCPTHS 300
DB 241 EAENSPPRMHCSAGEWLVPIGKCI CKAQYQKGDTPCEGRRTYKSSSDLOCRCPTHS 300
QY 301 FSPREGSSRCECDGYYRAPSDPYVACTRPPSAPOULININQTTVSLKASPADNGCR 360
DB 301 FSPREGSSRCECDGYYRAPSDPYVACTRPPSAPOULININQTTVSLKASPADNGCR 360
QY 361 NDVTYRILCKRCQWEGECVPCGSGNIGYMPQOTGLEBDNYTVNDLAHANYTEVEAVNG 420
DB 361 NDVTYRILCKRCQWEGECVPCGSGNIGYMPQOTGLEBDNYTVNDLAHANYTEVEAVNG 420
QY 421 VSDLSRSQRLFAAVSITTTGQAAPSOVSGWKEKERYLQSRVQLSQWQEPHPGVITTEYIKY 480
DB 421 VSDLSRSQRLFAAVSITTTGQAAPSOVSGWKEKERYLQSRVQLSQWQEPHPGVITTEYIKY 480
QY 481 YEKQDRERTYSTLTKTSTASINNLKPGTYVFOIRAVTAAGYNSPRIDVATLLEBASG 540
DB 481 YEKQDRERTYSTLTKTSTASINNLKPGTYVFOIRAVTAAGYNSPRIDVATLLEBASG 540
QY 541 KMEEATAVSSEQNPVIIIAVAVAGTIIIVFWVFGFIIIRRHGCGSKADGDBELYFHS 600
DB 541 KMEEATAVSSEQNPVIIIAVAVAGTIIIVFWVFGFIIIRRHGCGSKADGDBELYFHS 600
QY 601 LYREKDGMEKTOHKKMMIASCSRL 626
DB 601 LYREKDGMEKTOHKKMMIASCSRL 626

RESULT 2
ID AAW03422 standard; protein; 610 AA.

XX AAW03422;
XX
XX 11-NOV-1996 (first entry)
XX

DE Mouse developmental kinase 1 MDK1 T1.
XX
XX Mouse developmental kinase 1; MDK1 T1; receptor tyrosine kinase; RTK;
XX signal transduction; probe; diagnosis; gene therapy; neurodegeneration;
XX neuroproliferation; cancer.
XX
XX Mus sp.
XX
XX
FH Key Location/Qualifiers
FT Peptide 1..28 /label= Sig_peptide
FT Modified-site 64..66 /label= N-glycosylation_site
FT Modified-site 343..345 /label= N-glycosylation_site
FT Modified-site 410..412 /label= N-glycosylation_site
FT Domain 555..579 /label= Transmembrane_domain
FT Misc-difference 600..610 /note= "Product of alternative splicing"
FT
FT
PN MO9621013-A1.

XX 11-JUL-1996.
XX
XX 03-JAN-1996; 96WO-US000419.
XX
XX 03-JAN-1995; 95US-00368776.
XX
XX (SUGR-) SUGEN INC.
XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
XX Closek T, Ullrich A, Millaer B;
XX
XX WPI, 1996-333988/33.
XX
XX N-PSDB; AAT32961.

DR New mouse development kinase 1 gene - used for developing prods. for
DR diagnosis and treatment of abnormalities in signal transduction pathways.
XX
XX
XX
XX
XX
XX
PS Example 1; Page 109-111; 128bp; English.

XX CDNA cloning using adult mouse brains and Northern blotting identified 2
XX truncated versions, MDK1 T1 (AAW03422) and MDK1 T2 (AAW03423), of the
XX novel mouse developmental kinase 1 (MDK1) (see also AAW03421), a new
XX member of the eck/eph family of receptor tyrosine kinases. Their amino
XX acid sequences were deduced from cDNA clones (AAT32961 and AAT32962)
XX obtd. from adult mouse brains. MDK T1 and T2 each possess the entire
XX ectodomain, the transmembrane domain and part of the juxtamembrane region
XX of MDK1, but lack the catalytic tyrosine kinase domain. They can be used
XX to screen for potential agents useful for treatment of diseases
XX characterised by abnormal signal transduction
XX
XX
XX Sequence 610 AA:

Query Match 95.8%; Score 3199; DB 2; Length 610;
Best Local Similarity 100.0%; Pred. No. 2.6e-276; Mismatches 0; Indels 0; Gaps 0;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTQTFPSPWIIICYIWLGFAGTGAQAQAEVLLDLSKAQOTELEWISSPSGWEISG 60
DB 1 MVTQTFPSPWIIICYIWLGFAGTGAQAQAEVLLDLSKAQOTELEWISSPSGWEISG 60
QY 61 LDENYPIRTYQVCQWEPNQNMLRTNWSKGNARIFVELKFTLRDQNSLPGVIGTCK 120
DB 61 LDENYPIRTYQVCQWEPNQNMLRTNWSKGNARIFVELKFTLRDQNSLPGVIGTCK 120
QY 121 EFTNLYYYETDYGIRNIRENLVYKIDITIADESFTQDGLGERKMKLNTVEIREIGPLSKK 180
DB 121 EFTNLYYYETDYGIRNIRENLVYKIDITIADESFTQDGLGERKMKLNTVEIREIGPLSKK 180
QY 181 GFYLAFOVDGACIALVSVKYYKKCWTIVENLAVFPDVTGSEFSSLVEVRGTCVSSAAE 240
DB 181 GFYLAFOVDGACIALVSVKYYKKCWTIVENLAVFPDVTGSEFSSLVEVRGTCVSSAAE 240

XX Human protein SEQ ID NO:260.
 DE
 XX
 XX
 KM respiratory; cytoskeletal; antiarthritic; immunosuppressive; antidiabetic;
 KM gastrointestinal; antibacterial; immunosuppressive; antidiabetic;
 KM antineuritic; gene therapy; molecular weight marker; chromosome marker;
 KM chromosome tag; genetic fingerprinting; nutritional supplement; cancer;
 KM inflammatory condition; arthritis; inflammatory bowel disease;
 KM Crohn's disease; sepsis; rheumatoid arthritis; diabetes mellitus type 1;
 KM graft versus host disease; human.
 XX
 OS Homo sapiens.
 PN MO2004009834-A2.
 XX
 XX 29-JAN-2004.
 PD
 XX
 PF 19-JUL-2002; 2002MO-US022858.
 XX
 XX 21-JUL-2001; 2001US-0306971P.
 PR 28-MAR-2002; 2002US-00112944.
 XX
 PA (NUVE-) NUTVELO INC.
 XX
 PI Tang YT, Yang Y, Weng G, Zhang J, Ren F, Xue A, Wang J;
 PI Wehrman T, Ghosh MJ, Wang D, Zhao QX, Wang Z;
 XX
 DR WPI; 2004-143291/14.
 N-PDB; ADM66923.
 XX
 XX
 PT New isolated polynucleotides and polypeptides, useful for treating, e.g.
 PT cancer, lung or liver fibrosis, arthritis, inflammatory bowel disease,
 PT Crohn's disease, rheumatoid arthritis, diabetes mellitus type 1 or graft
 PT versus host disease.
 XX
 PS Claim 20; SEQ ID NO 260; 591pp; English.
 XX
 CC The present invention describes an isolated polynucleotide (I): (a)
 CC comprising a nucleotide sequence selected from SEQ ID NO:1-344; or (b)
 CC which encodes a polypeptide with biological activity, where the
 CC polynucleotide hybridises to (I) under stringent hybridisation conditions
 CC or has greater than 99% sequence identity with (I). (I) has respiratory,
 CC cytoskeletal, antiarthritic, antiinflammatory, gastrointestinal,
 CC antibacterial, immunosuppressive, antidiabetic and antineuritic
 CC activities, and can be used in gene therapy. (I) can be used for
 CC generating polynucleotides encoding chimeric or fusion proteins and
 CC heterologous protein sequences. The polynucleotides can be used to
 CC express recombinant protein for analysis, characterisation or therapeutic
 CC use; as markers for tissues in which the corresponding protein is
 CC preferentially expressed; as molecular weight markers on gels; as
 CC chromosome markers or tags to identify chromosomes or to map related gene
 CC positions; to compare with endogenous DNA sequences in patients to
 CC identify potential genetic disorders; as probes to hybridise and discover
 CC gene, related DNA sequences; as a source of information to derive PCR
 CC primers for genetic fingerprinting; as a probe to substract-out known
 CC sequences in the process of discovering other novel polynucleotides; for
 CC selecting and making oligomers for attachment to a gene chip or other
 CC support, including for examination of expression patterns; to raise anti-
 CC protein antibodies using DNA immunisation techniques; and as an antigen
 CC to raise anti-DNA antibodies or elicit another immune response. The
 CC polynucleotides and polypeptides can also be used as nutritional sources
 CC or supplements, e.g. as a protein or amino acid supplement, as a carbon
 CC source, as a nitrogen source or as a source of carbohydrates. The
 CC polynucleotides and polypeptides can also be used treat cancer. The
 CC compositions are useful for promoting better or faster closure of non-
 CC healing wounds, for the generation and regeneration of tissues, for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, and conditions resulting from
 CC systemic cytokine damage. The compositions can also be used to treat
 CC inflammatory conditions (e.g. arthritis, inflammatory bowel disease or
 CC Crohn's disease), sepsis, rheumatoid arthritis, diabetes mellitus type 1
 CC or graft versus host disease. The present sequence represents a novel
 CC human polypeptide sequence from the present invention. N.B. The sequences

CC for this patent were obtained from the USPTO web site from an equivalent
 CC US patent US20040048249A1.
 XX
 CC
 XX Sequence 945 AA;
 SQ
 Query Match 94.0%; Score 3139; DB 8; Length 945;
 Best Local Similarity 97.7%; Pred. No. 1,2e-270;
 Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MVTQTFPSMIIICVYTWLGFPAHTGEAQAKEYLLDLSAAQOTELMISPPSGMEISG 60
 DB 1 MVTQTFPSMIIICVYTWLGFPAHTGEAQAKEYLLDLSAAQOTELMISPPSGMEISG 60
 QY 1DENYTPIRTYGVCQWMEPNQNNWLTNNISKNAQRIVELKFTLRDQNSLPGVIGTCK 120
 DB 1DENYTPIRTYGVCQWMEPNQNNWLTNNISKNAQRIVELKFTLRDQNSLPGVIGTCK 120
 QY 121 EFTNLYYYETDPTDGTGNIRENLVYKIDTAADESFQDGLGERKMLNTEVRIGPLSKK 180
 DB 121 EFTNLYYYETDPTDGTGNIRENLVYKIDTAADESFQDGLGERKMLNTEVRIGPLSKK 180
 QY 181 GFYLAFOYDQACIALSVKYYKKCWTIVENLAVPDTYGSFSSLVEVRGTCVSSAE 240
 DB 181 GFYLAFOYDQACIALSVKYYKKCWTIVENLAVPDTYGSFSSLVEVRGTCVSSAE 240
 QY 241 EAENSBRMHCASAEGLWLVPIGKICIKAGYQKQDTCPCGRFRYKSSSODLQSCRPTHS 300
 DB 241 EAENSBRMHCASAEGLWLVPIGKICIKAGYQKQDTCPCGRFRYKSSSODLQSCRPTHS 300
 QY 301 FSDRESSSRCECDGYRPAAPDPYACRPPSAPQNLFINQTTVSLWSPPADNGR 360
 DB 301 FSDRESSSRCECDGYRPAAPDPYACRPPSAPQNLFINQTTVSLWSPPADNGR 360
 QY 361 NDVTYRIILCKRCSEWEGCEVPCGSNIGVMPQDTGLENDVTYWDLLAHNYTFEVAVNG 420
 DB 361 NDVTYRIILCKRCSEWEGCEVPCGSNIGVMPQDTGLENDVTYWDLLAHNYTFEVAVNG 420
 QY 421 VSDLSRSQRLFAVSLTTGQAAPSQVGVKKEVILQSVLSQWEPHNGVITEYIKY 480
 DB 421 VSDLSRSQRLFAVSLTTGQAAPSQVGVKKEVILQSVLSQWEPHNGVITEYIKY 480
 QY 481 YENDQGERYTYLTKTSTASINLKPQVYVYQIRPAVAAAGVNSPPLDVATLEAAG 540
 DB 481 YENDQGERYTYLTKTSTASINLKPQVYVYQIRPAVAAAGVNSPPLDVATLEAAG 540
 QY 541 KMFEATAVSSEQNPVLIIVAVAGTIIIVFWFGFIIGRRHCGYSKADQEGDELYFH 599
 DB 541 KMFEATAVSSEQNPVLIIVAVAGTIIIVFWFGFIIGRRHCGYSKADQEGDELYFH 599
 RESULT 5
 ID AAR85092
 XX AAR85092 strand; protein; 998 AA.
 AC AAR85092;
 XX
 XX 16-APR-1996 (first entry)
 DT
 XX
 DE BPH-like receptor protein tyrosine kinase HEK11.
 KW BPH-like receptor protein tyrosine kinase; PK; HEK11;
 KW human eph-like kinase; therapy; diagnosis; antibody; vector.
 OS Homo sapiens.
 XX
 PN MO9528484-A1.
 XX
 PD 26-OCT-1995.
 XX
 PF 14-APR-1995; 95WO-US004681.
 XX
 PR 15-APR-1994; 94US-00229509.
 XX

PA (AMGE-) AMGEN INC.
 XX Fox GM, Welcher AA, Jing S;
 XX WPI; 1995-373799/48.
 DR N-PSDB; AAT02949.
 XX
 PT New nucleic acid encoding EPH-like receptor tyrosine kinase(s) - and
 PT related vectors, host cells, proteins, antibodies etc., used
 PT diagnostically and therapeutically to modulate receptor activation or
 PT prodn.
 XX
 PS Claim 18; Page 71-75; 133pp; English.
 XX
 CC 4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7,
 CC HEK8 and HEK11 (AAR85089-92), respectively, were identified following
 CC isolation of their encoding cDNAs (AAT02946-49) from a human foetal brain
 CC cDNA library. HEK5, HEK7 and HEK8 show extensive homology to the
 CC catalytic domain of chicken EPH-like receptors Cek5, Cek7 and Cek8. HEK11
 CC shows no homology to any known EPH-like receptor. Recombinant HEK
 CC receptors (or their soluble extracellular domains) are produced by
 CC expression of encoding sequences in prokaryotic or eucaryotic host cells,
 CC and are used to produce antibodies (utilised in diagnostic assays), or to
 CC identify and purify ligands for HEK receptors, or therapeutically to
 CC modulate the activation of cell-associated receptors
 CC
 XX Sequence 998 AA:
 SQ
 Query Match 94.0%; Score 3139; DB 2; Length 998;
 Best Local Similarity 97.7%; Pred. No. 1.3e-270;
 Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MVNQTREFSWIIICYLWLGFAHNGEAAKEVILLDSKAQOTLEWISSPPSGWEIISG 60
 DB 1 MFGTRYPSSWIIICYLWLRPAHNGEAAKEVILLDSKAQOTLEWISSPPNGEIEISG 60
 QY 61 LDEVTPIRTYOVCOVMEPNONMMLRTMWSKGNORIFVELKFTLRDONSIPVGLGTCK 120
 DB 61 LDEVTPIRTYOVCOVMEPNONMMLRTMWSKGNORIFVELKFTLRDONSIPVGLGTCK 120
 QY 121 ETFNLYYETDYGTRNIRENLYVKIDTIADESFTQGDIGERRKMKLNTVEIREIGPLSKK 180
 DB 121 ETFNLYYETDYGTRNIRENLYVKIDTIADESFTQGDIGERRKMKLNTVEIREIGPLSKK 180
 QY 181 GFYLAFOVGACIALVSKYVYKCKWTIVENLAVPPTVTGSSBSLVEVGTGVSSABE 240
 DB 181 GFYLAFOVGACIALVSKYVYKCKWTIVENLAVPPTVTGSSBSLVEVGTGVSSABE 240
 QY 241 EAENSPRMHCAGEBMLVPIGKICIKAGYQOKGDTCECGRRFYKSSSODLQCSRCPHIS 300
 DB 241 EAENSPRMHCAGEBMLVPIGKICIKAGYQOKGDTCECGRRFYKSSSODLQCSRCPHIS 300
 QY 301 FSDREGSSRCCEBDGYRAPSDPPVACTRPPSAPONLIFINOTTVSLEWSPPADNGR 360
 DB 301 FSDREGSSRCCEBDGYRAPSDPPVACTRPPSAPONLIFINOTTVSLEWSPPADNGR 360
 QY 361 NDVYTRILCKRCMEQECVPCGSNIGYMPQOTGLEDDYVYVMDLAAANTFFEEAANG 420
 DB 361 NDVYTRILCKRCMEQECVPCGSNIGYMPQOTGLEDDYVYVMDLAAANTFFEEAANG 420
 QY 421 VSDLSRSORLFAAASITTGGAAPSOVSGVMKERVQSRVOLSWOBEHPHNGVITEYEIKY 480
 DB 421 VSDLSRSORLFAAASITTGGAAPSOVSGVMKERVQSRVOLSWOBEHPHNGVITEYEIKY 480
 QY 481 YEKQRERTYSTLTKTSTASINNLKPGTVYVFOIRAYTAAGYGNYSRDLVATLEASG 540
 DB 481 YEKQRERTYSTLTKTSTASINNLKPGTVYVFOIRAYTAAGYGNYSRDLVATLEASG 540
 QY 541 KMFEATAVSSRONPITIIAAVAVAGTIIIVFVVFEGIIIGRRHCGSKADQGBDELYPH 599
 DB 541 KMFEATAVSSRONPITIIAAVAVAGTIIIVFVVFEGIIIGRRHCGSKADQGBDELYPH 599

RESULT 6
 AAR85090
 ID AAR85090 standard; protein: 991 AA.
 XX
 AC AAR85090;
 XX
 DT 16-APR-1996 (first entry)
 XX
 DE EPH-like receptor protein tyrosine kinase HEK7.
 XX
 KM EPH-like receptor protein tyrosine kinase; PT; HEK7.
 KM human eph-like kinase; therapy; diagnosis; vector; antibody.
 XX
 OS Homo sapiens.
 XX
 PN W09528484-A1.
 XX
 PD 26-OCT-1995.
 XX
 PF 14-APR-1995; 95WO-US004681.
 XX
 PR 15-APR-1994; 94US-00229509.
 XX
 PA (AMGE-) AMGEN INC.
 PI Fox GM, Welcher AA, Jing S;
 XX
 DR WPI; 1995-373799/48.
 DR N-PSDB; AAT02949.
 XX
 PT New nucleic acid encoding EPH-like receptor tyrosine kinase(s) - and
 PT related vectors, host cells, proteins, antibodies etc., used
 PT diagnostically and therapeutically to modulate receptor activation or
 PT prodn.
 XX
 PS Claim 18; Page 54-57; 133pp; English.
 XX
 CC 4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7,
 CC HEK8 and HEK11 (AAR85089-92), respectively, were identified following
 CC isolation of their encoding cDNAs (AAT02946-49) from a human foetal brain
 CC cDNA library. HEK5, HEK7 and HEK8 show extensive homology to the
 CC catalytic domain of chicken EPH-like receptors Cek5, Cek7 and Cek8. HEK11
 CC shows no homology to any known EPH-like receptor. Recombinant HEK
 CC receptors (or their soluble extracellular domains) are produced by
 CC expression of encoding sequences in prokaryotic or eucaryotic host cells,
 CC and are used to produce antibodies (utilised in diagnostic assays), or to
 CC identify and purify ligands for HEK receptors, or therapeutically to
 CC modulate the activation of cell-associated receptors. Soluble HEK7
 CC receptor may primarily affect cell proliferation and/or differentiation of
 CC brain cells. pancreatic cells
 CC
 XX Sequence 991 AA:
 SQ
 Query Match 55.2%; Score 1841; DB 2; Length 991;
 Best Local Similarity 57.4%; Pred. No. 1.4e-154;
 Matches 345; Conservative 97; Mismatches 133; Indels 26; Gaps 8;
 QY 6 RFPSSW--IILCYWLGFAHNGEAAKEVILLDSKAQOTLEWISSPPSGWEIISGIDE 63
 DB 13 RAPLMTCILLC-----AALRTLLASPSNEVILLDSRTVMGLGVIAPPKMMEBIGEYDE 67
 QY 64 NYTPIRTYOVCOVMEPNONMMLRTMWSKGNORIFVELKFTLRDONSIPVGLGTCKETF 123
 DB 64 NYTPIRTYOVCOVMEPNONMMLRTMWSKGNORIFVELKFTLRDONSIPVGLGTCKETF 127
 QY 124 NLVYETDYGTRNIRENLYVKIDTIADESFTQGDIGERRKMKLNTVEIREIGPLSKKGFY 183
 DB 128 NMVYFSDPDQNGRNIRKNOYIKIDTIADESFTLDDGRVMKLNTEVROVGPLSKKGFY 187
 QY 184 LAFODVGACIALVSKYVYKCKWTIVENLAVPPTVTGSSBSLVEVGTGVSSABEAB 243
 DB 188 LAFODVGACIALVSKYVYKCKPSVVRHLAVFPDITIGADSSQLLEVSGSCVN--HSVTD 245

```

QY      244 NSPRHNCSEBGMVLPIGICTCKAGYQOKGDTPCGRFRFYKSSQDLQCSRPCTHSFSD 303
QY      246 BPPKHCSEBGMVLPIGICKMCKAGYEENKGTQYVCRPGFFKASPHIOSGCKCPHSHYTH 305
Db      246 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      304 REGSSRCEDEDEYTPASDPDYVACRPPSAPONLIFINIOCTVSLFEMSPALCNGENDV 363
QY      306 BEASISCYCEKRYFRESDEPTMACRPPSAPRNALSNVEISVFLFEMIPALGTGRKDV 365
Db      364 TYRILCKRCSWEQECVPCGSGNIYMPQOTGLENDYVTLMDLLAANYTTEVAANGVSD 423
QY      366 SYVILCKKNCNSHAGVCECGGHVRYLPROSGLKNITSVMVMDLLAHTNYTTEIANGVSD 425
Db      424 LSRGRLPAFVSIITGGQAPSPQVSGMKERVLORSQLSMQEPHENGVITFEIKTYEK 483
QY      426 LSPGARQYVAVVTTNQAAPSPVTVNKKIKKIANKSISLSMQEEDRPNGIILEYIKHFEK 485
Db      484 DORERTVSTLTKRSTYSASINNLKPGTVVYFOIARVAAGAAGNSPRLDVTLEBASGMF 543
QY      486 DO-EISYTIKKEKETTITTEGLKPAVSYYFOIARPAAGAGVSRPE-----F 533
Db      544 EAT---AVSSEONPVIIILVAVVAGTIIIVFMVGFPIIGRRHGYSKADCEGDEE-LYFH 599
QY      534 ETTVPFAASSDQSQIPVIIVASTVG-VILLAVIIGVLLSGRRGYSKAKCDPEBEKMHFH 592
QY      600 S 600
Db      593 N 593

```

| | |
|----------|---|
| RESULT 7 | |
| ABP52826 | |
| ID | ABP52826 standard; protein, 953 AA. |
| XX | |
| AC | ABP52826; |
| XX | |
| DT | 31-OCT-2002 (first entry) |
| XX | |
| DE | Human receptor protein-tyrosine kinase SEQ ID NO:7. |
| XX | |
| KW | Human; kinase; enzyme; inflammation; cancer; psoriasis; gene therapy; |
| KW | arteriosclerosis; antiinflammatory; cytosstatic; antipsoriatic; |
| KW | antiarteriosclerotic. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| PN | WO200257432-A2. |
| PD | |
| XX | 25-JUL-2002. |
| XX | |
| PF | 02-JAN-2002; 2002WO-US000112. |
| XX | |
| PR | 02-JAN-2001; 2001US-00751389. |
| XX | |
| PA | (PEKE) PE CORP. |
| XX | |
| P1 | Guegler K, Webster M, Di Francesco V, Beasley EM; |
| XX | |
| DR | WPI; 2002-599718/64. |
| PT | |
| PT | New peptides encoded by genes within the human genome useful for treating |
| PT | disorders associated with abnormal expression of kinase, e.g. |
| PT | inflammation, cancer, arteriosclerosis, in drug screening assays and |
| PT | pharmacogenomic analysis. |
| XX | |
| XX | |
| PS | Disclosure; Fig 2G-H; 346pp; English. |
| XX | |
| CC | |
| CC | The present invention describes a human kinase protein (I), located on |
| CC | chromosome 3. (I) has antiinflammatory, cytostatic, antiproliferatic and |
| CC | antiarteriosclerotic activities, and can be used in gene therapy. (I) |
| CC | peptides can be used in substantial and specific assays related to |
| CC | functional information of the peptide sequences, to raise antibodies or |
| CC | to elicit immune response, as reagents in assays to determine the levels |
| CC | of protein in biological fluids, and as markers for tissues where the |

CC corresponding protein is expressed. The peptides and antibodies are
CC useful in drug screening assays, tissue typing and pharmacogenomic
CC analysis. They are also useful in treating disorders associated with the
CC absence of, inappropriate, or unwanted expression of the kinase protein,
CC e.g. inflammation, cancer, arteriosclerosis, and psoriasis. The nucleic
CC acid molecules encoding (I) can be used for probes, primers and chemical
CC intermediates in biological assays, for constructing recombinant vectors,
CC expressing antigenic portions of the protein. The peptide and nucleic
CC acid sequences are useful as models for the development of human
CC therapeutic targets, aid in the identification of therapeutic proteins
CC and serve as targets for the development of human therapeutic agents that
CC modulate kinase activity in cells and tissues that express the kinase.
CC The present sequence represents a protein given in comparison with the
CC human kinase protein of the present invention
XX
SQ Sequence 953 AA;

| Query Match | 54.8% | Score 1830.5 | DB 5 | Length 953 |
|--------------------------------------|--|--|-----------|------------|
| Best Local Similarity | 58.8% | Fred. No. 1.1e-153 | | |
| Matches 338 | Conservative 95 | Mismatches 123 | Indels 19 | Gaps 6 |
| QY | 30 | AKEVLLDSSKAOQEELEWISSPPSGMEBISGLDENYRTYRTYQVCQVMEPNQNNMLRTNM | 89 | |
| DB | 1 | SNEVNLDSRIVMDEGLGIAFPKNGMEBIGEVDENYAIPHYYQCKWMEQNNMMLLSW | 60 | |
| QY | 90 | ISKNGAQRIFVELKFTLRDCHSLPGVLGCTCKETFNLYYEFDYDGRNIRENLYIKIDTI | 149 | |
| DB | 61 | ISNGASRIFIELEKFTLRDCHSLPGGLGCTCKETFNMYFEEDDDGNRIKENQYIKIDTI | 120 | |
| QY | 150 | AADESFQGDGGERGMRKNTREVRLEIGPLSKSGFLAFQDVACIALVSVKYYKKCWITV | 209 | |
| DB | 121 | AADESFTELDGDMKLTREVRDVGPLSKSGFLAFQDVACIALVSVRYYYKKCPSVV | 180 | |
| QY | 210 | ENLAVFPDVTGTGSEBSSILVEVRGTGVSSAEBAENS PMHCSABGEMLVPIGCKI CKAGY | 269 | |
| DB | 181 | RHLAVFPDVTITGADSSQLLEVSGSCVN--HSVTDEPPMHCSABGEMLVPIGCKMCKAGY | 238 | |
| QY | 270 | QOKGDTGCPGCRRRPYKSSODLOSRCTPSFSDREGSSRCEGCEGYRASPDPVYACT | 329 | |
| DB | 239 | EKKNGTCOVCPRGFFPKSPHIOGSGKCPPHSYTHREASTCVCEKDYIRRESDPPTMACT | 298 | |
| QY | 330 | RPSAPQNTLPINQTTVSLSEWSPADNGRNDYTYRLICKRCSEWGEVCVPCGSNIGYM | 389 | |
| DB | 299 | RPPAPRRAISNVNETSVELEWIRPADTGGRKDDYYIACKCKMSHAGVCECGHVVYL | 358 | |
| QY | 390 | POOGLENDNYTWDMLAHANYTEVEVAVNVNSLSRSORFLFAVSYITGGAASQVSGV | 449 | |
| DB | 359 | PROGLKNTSVMMQDLAHNYTEIEIKVNVNSDLSPEARQYVSNVYTNQDAASPVNV | 418 | |
| QY | 450 | MKEVLORSVOLSWOEPEHPNGVITEYEIKYKEXDORERTYSTLKTSASINNLKPGT | 509 | |
| DB | 419 | KKGIARKNSISLSWOEPDRPGIILLEYEIKHFEKDO--ETSYTIKSKETTYTAAGLKPAS | 477 | |
| QY | 510 | VYVVOIQAIVTAAGGNVSPRLDVATLEASAKMEAT---AVSSEQNVIILAAVAVAGT | 566 | |
| DB | 478 | VYVVOIRRRTIAGVGVSRRE-----FETTPVFASSDQSOIPIAVSVTVG- | 525 | |
| QY | 567 | IILVFMVFGFIIGRRHCGSKADQEGDEE-LYFHS 600 | | |
| DB | 526 | VILLAVVIGVLSGRRCGYSKAKDDPEEKKHFFLN 560 | | |
| RESULT 8 | | | | |
| AAW83147 standard; protein; 1005 AA. | | | | |
| XX | AAW83147 | | | |
| XX | AAW83147; | | | |
| XX | 11-FEB-1999 (first entry) | | | |
| XX | Rat receptor tyrosine kinase Ehk-1. | | | |
| XX | Receptor tyrosine kinase; Ror-1; Ror-2; Ehk-1; Ehk-2; detection; | | | |

KM neurotrophin activity; trkB; proto-oncogene; tyrosine kinase receptor;
 KM binding protein; BDNF; NT-3; diagnosis.
 XX Rattus sp.
 OS US5843749-A.
 XX PN
 XX PD 01-DEC-1998.
 XX PF 06-JUN-1995; 95US-00469537.
 XX PR 26-JUL-1991; 91US-00736559.
 PR 28-OCT-1993; 93US-00144992.
 PR 17-MAR-1995; 95US-00406247.
 XX PA (REG-) REGENERON PHARM INC.
 XX PI Maslakowski P, Yancopoulos GD, Maisompierre PC;
 XX WPI: 1999-044584/04.
 DR N-PSDB; AAV70207.
 XX PT DNA encoding receptor tyrosine kinase proteins - and corresponding
 PT proteins.
 XX PS Example; Fig 22; 194pp; English.
 XX CC The present invention describes nucleic acid molecules for *ror-1*, *ror-2*,
 CC *ehk-1* and *ehk-2*. Also described are the corresponding proteins: *Ror-1*,
 CC *Ror-2*, *Ehk-1*, and *Ehk-2*. The proteins are orphan receptor tyrosine
 CC kinases. The present sequence represents rat *Ehk-1*.
 XX CC
 SQ Sequence 1005 AA;

Query Match 54.6%; Score 1822; DB 2; Length 1005;
 Best Local Similarity 55.2%; Pred. No. 7.1e-153;
 Matches 349; Conservative 95; Mismatches 136; Indels 52; Gaps 10;

QY 6 RFPSEWILCY-----IM-----LLGFHNGEAQAKEYVLLDSKAQOTLEWISSPPSG 54
 DB 25 RVPASLAGCTYSAPLKPGPLMTCLLCAALRTLLASPSNEVLLDSRTVLDGWIAPKNG 84
 QY 55 WEBSIGLDENTYPTRTYOVQVMEPNONNMRLTWMISKGNARIFVELKFTLRDQNSLPG 114
 DB 85 WEBSIGEDENYAPRHTYOVCKVMEONONMRLTWMISSEGSRIFFELKFTLRDQNSLPG 144
 QY 115 VLGTCKETPNLYYETDYDTGRNIRENLYKIDITIADESFTQDLGERKKNLTYEREI 174
 DB 145 GLGTCKETPNMYYPESDDENGRNIRENOYIKIDITIADESFTBLDGRVKNLTYERADV 204
 QY 175 GPLSKGFYLAFOVGACIALVSVKYYKKWTIVENLAVPDPVTGSEFSLVEVWGTC 234
 DB 205 GPLSKGFYLAFOVGACIALVSVKYYKKCPVVRHLAVPDPVTGADSSQLLEVSGSC 264
 QY 235 VSSAEBAENSPRMAAGSEGLVPIGKICAKAGYQKGDCECGRRFYSSSODLQCS 294
 DB 265 VN--HSTYDDPRKXHCAGEMLVPIGCKCKAEEENGCYQCRPFASFHSQTCS 322
 QY 295 RCPHSPSDBREGSSRCECEGYRAPSDDPYVACTRPPSAPDNLIPINQTTVSLWSP 354
 DB 323 KCPHSTHHEASTSCVCEKDYFRRESPPPMACTRPPSAPRANISVNETSVLEWIP 382
 QY 355 ADNGRNDYRILICXKCSWEGECVPCGSNIGMPOGTGLEDYVYVMDLAAANTFE 414
 DB 383 ADTGKQDVSYILLCKKCNHAGVCEGCGHVRLLPOOIGLKNISVMDADLAAHTNTEFE 442
 QY 415 VEAANGVDSLRSORLFAAVSITGQAAPSOVSGVMKEVYQSRVQSLWQEPHPNGVIT 474
 DB 443 IEANGVSDLSPGRQYVSVVTTNOAAPSPVTYVKKIKAKNISLSWQEPDPNNGIIL 502
 QY 475 EYEIKYKQDERRTYTLTKYSTASINNLKPGTVYVFOIRAVTAAGYNGYSPRLDVA 534
 DB 503 EYEIKYFEKQD-ETSYITIKSKETTLTAEGIKPASVYVFOIRARTAGYGVSRFRFE-- 558

QY 535 LEEASGKFEATAY---SSEONPYIIAAVAVAGTILVEMVGFII-----GRR- 581
 DB 559 -----FETTPYFGASNDOSQIPITIGSVTVGVILAAWI-GFLSSGCECGCGRAS 609
 QY 582 -----HCGYSKADQEGDEE-LYFHS 600
 DB 610 SLCAVAHPSLIWRCGYSKAKODPEEKQMFHN 641

RESULT 9
 ABR44241
 ID ABR44241 standard; protein; 1037 AA.
 XX AC ABR44241;
 XX XX 18-AUG-2003 (first entry)
 XX DT
 XX DE Tyrosine kinase EHK-1.
 XX KM CD81; neuron; neural degeneration; astrocyte; Nrs1; cytosolic; EHK-1;
 KM neuroprotective; nootropic; antiparkinsonian; anticonvulsant; human;
 KM cerebroprotective; gene therapy; tyrosine kinase.
 XX OS Homo sapiens.
 XX PN WO2003040333-A2.
 XX XX 15-MAY-2003.
 XX PD 07-NOV-2002; 2002MO-US035588.
 XX PR 07-NOV-2001; 2001US-0344712P.
 XX PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.
 XX PI Weinstein DE, Suarez C, Zerlin M;
 XX WPI: 2003-441557/41.
 DR N-PSDB; ACC78163.
 DR XX
 PT Enhancing survival of neurons, useful for treating neural degeneration
 PT (e.g. Alzheimer's disease) or a defect in astrocyte proliferation (e.g.
 PT astrocytosis), comprises contacting the neurons with CD81 protein or its
 PT derivative.
 XX PS
 PS Claim 29; Fig 28; 59pp; English.
 CC The invention relates to enhancing survival of neurons and involves
 CC contacting the neurons with CD81 protein or CD81 derivative, or its
 CC stabilized variants, in an amount that enhances survival of the neurons.
 CC The method is useful for treating neural degeneration or a condition
 CC associated with a defect in astrocyte proliferation in a mammal, and
 CC involves activating Nrs1 or CD81 in the mammal. The method is useful in
 CC treating neural degeneration (e.g. Alzheimer's disease, amyotrophic
 CC lateral sclerosis, Binswanger's disease, Huntington's chorea, multiple
 CC sclerosis, myasthenia gravis, Parkinson's disease, Pick's disease,
 CC cerebral palsy, congenital hydrocephalus, muscular dystrophy, stroke or
 CC vascular dementia) or a condition associated with a defect in astrocyte
 CC proliferation, such as astrocytosis or astrocytoma. The present sequence
 CC represents a the EHK-1 protein (the Nrs1 protein has been previously
 CC identified as an orphan receptor tyrosine kinase termed EHK-1 -GenBank
 CC Accession No. XM_046083.2.)
 CC XX
 SQ Sequence 1037 AA;

Query Match 54.6%; Score 1822; DB 6; Length 1037;
 Best Local Similarity 55.7%; Pred. No. 7.4e-153;
 Matches 347; Conservative 96; Mismatches 132; Indels 48; Gaps 10;

QY 6 RFPSEW--IILCYWLLGFHNGEAQAKEYVLLDSKAQOTLEWISSPPSGWEISGLDE 63
 DB 37 RAPLMTCLILC-----AALRTLLASPSNEVLLDSRTVMGDLQWIAFPKNGWEISGRVDE 91


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QY 64 NYTPIRTYOQVMEPNQNNMLRTNWSKGNARIFVELKFTLRDNCNSLPGLGTCKETP 123
DB 92 NYAPRHTYQVCKMEQNNWMLTWSINSGASRIFFELKFTLRDNCNSLPGLGTCKETP 151
QY 124 NLYYEFDVDTGRNIRENLVYKIDTIADESFTQDGERKMKLNTVEIREI3PSKKGFF 183
DB 152 NMYYFESDDQNGRNIRENOYIKIDTIADESFTELDGDVYMKLNTVEIRV3PLSKKGFY 211
QY 184 LAFQDVACIALVSVKYYKKCMWTIENLAVFPDVTGSEFSSLVREYRGCVSSAEBAE 243
DB 212 LAFQDVACIALVSVRYKKCEVVRHLAVFPDTITGADSSQLLEVSGSCVN--HSVTD 269
QY 244 NSPRMCSAEGEVLVPIGKICCKAGYQOKDTCPCGRFRFYKSSODLQCSRCPHSFSD 303
DB 270 EPPRMCSAEGEVLVPIGKICCKAGYBEKNGTCQVCRPFGRFKASPHIQSCGKCPHSYTH 329
QY 304 REGSSRECEDEGYRAASDPYVACTPPSAPQNLININQTTVLSWSPADNGGRNDV 363
DB 330 EEAATSCVCEKDYFRRESDPYVACTPPSAPRANLISNVETSVLEWIPFADTGGRKDV 389
QY 364 TYRILCKRCGMEQCEVPCGSNIGYMPQOTGLEDNVYVMDLLAHANYTFEEVAVNGVSD 423
DB 390 SYTIACKCKNSHAGVCECGHRYLPRQSGLKNTSVMMDLLAHNTYTFIEAVNGVSD 449
QY 424 LSRSORLFAAVSITTTQGAAPSOVSGVWKERVLORSVOLSMQEPHNGVITTEYIKYK 483
DB 450 LSPGARQYVSVNTTQGAAPSPVTNVKKGKIAKNSISLSWQEPDRPNGIILEYIKYFEK 509
QY 484 DQERTYSTLKTSTASINNLKGTYYVFOIRAVTAAGYNSPRLDVATLEASGKMF 543
DB 510 DQ-ETSYTIKSKETITTAGLKPASVYFOIRARTAGYGVFSRPE-----F 557
QY 544 EAT---AVSSEQNPVILIAVAVAGTIIIVMVFGFI-----GRR----- 581
DB 558 ETTVPFPAASDDQOIPVIAVSVTWG-VILAVVIGVLSSGCEGCGRAKSLCAVAHPS 616
QY 582 ---HGYSKADQEGDEE-LYFHS 600
DB 617 LWRGCGYKAKQDPEEEMHFNH 639

RESULT 10
ABG61868
ID ABG61868 standard; protein; 1037 AA.
AC ABG61868;
XX
DT 15-AUG-2002 (first entry)
XX
DE Prostate cancer-associated protein #69.
XX
KM Prostate cancer; prostate tumour tissue; human; mammal; cyclostatic.
XX
OS Mammalia.
XX
PN WO200230268-A2.
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001KO-US032045.
XX
PR 13-OCT-2000; 2000US-00687576.
PR 08-DEC-2000; 2000US-00733288.
PR 08-DEC-2000; 2000US-00733742.
PR 24-JAN-2001; 2001US-0263957P.
PR 16-MAR-2001; 2001US-0276791P.
PR 16-MAR-2001; 2001US-0276888P.
PR 06-APR-2001; 2001US-0281922P.
PR 24-APR-2001; 2001US-0286214P.
PR 30-APR-2001; 2001US-00847046.
PR 04-MAY-2001; 2001US-0286589P.
XX

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PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX WPI; 2002-471335/50.
DR N-PSDB; ABK92183.
XX
PT Detecting a prostate cancer-associated transcript in a cell in a patient,
PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,
PT by determining if prostate cancer-associated genes are expressed in a
PT prostate tissue.
XX
PS Claim 27, Page 354; 436pp; English.
XX
XX The present invention relates to methods of detecting a prostate cancer-
XX associated transcript in a cell from a patient. The method comprises
XX contacting a biological sample from the patient with prostate cancer-
XX associated polynucleotides (designated PC genes) that selectively
XX hybridize to a sequence that is at least 80% identical to them. The
XX prostate cancer-associated polynucleotide sequences are differentially
XX expressed in prostate tumour tissue or in prostate cancer and are derived
XX from the tissues of various organisms such as humans or other mammals
XX (e.g. mice, sheep and dogs). The methods of the invention are useful for
XX diagnosing and treating prostate cancer in mammals. The prostate cancer-
XX associated genes are useful for diagnosing or treating prostate cancer,
XX as well as for identifying modulators of prostate cancer or agents that
XX inhibit prostate cancer. The nucleic acid sequences are particularly
XX useful in gene therapy, as a vaccine or in antisense applications.
XX ABG61800-ABG61944 represent prostate cancer-associated proteins
XX
SQ Sequence 1037 AA;
Query Match 54.4%; Score 1817; DB 5; Length 1037;
Best Local Similarity 55.5%; Pred. No. 2,1e-152;
Matches 346; Conservative 97; Mismatches 132; Indels 48; Gaps 10;

QY 6 RFPSS--IILCYTWLGFPAHTGEAQAKEYLLDSQAQOLETEWISSPSSGWEIEIGLDE 63
DB 37 RAFLWTCLLCC-----AAURLTLASPSNEVNLDSRTVWGDLGWIAPKNGWEIEIYDE 91
QY 64 NYTPIRTYOQVMEPNQNNMLRTNWSKGNARIFVELKFTLRDNCNSLPGLGTCKETP 123
DB 92 NYAPRHTYQVCKMEQNNWMLTWSINSGASRIFFELKFTLRDNCNSLPGLGTCKETP 151
QY 124 NLYYEFDVDTGRNIRENLVYKIDTIADESFTQDGERKMKLNTVEIREI3PSKKGFF 183
DB 152 NMYYFESDDQNGRNIRENOYIKIDTIADESFTELDGDVYMKLNTVEIRV3PLSKKGFY 211
QY 184 LAFQDVACIALVSVKYYKKCMWTIENLAVFPDVTGSEFSSLVREYRGCVSSAEBAE 243
DB 212 LAFQDVACIALVSVRYKKCEVVRHLAVFPDTITGADSSQLLEVSGSCVN--HSVTD 269
QY 244 NSPRMCSAEGEVLVPIGKICCKAGYQOKDTCPCGRFRFYKSSODLQCSRCPHSFSD 303
DB 270 EPPRMCSAEGEVLVPIGKICCKAGYBEKNGTCQVCRPFGRFKASPHIQSCGKCPHSYTH 329
QY 304 REGSSRECEDEGYRAASDPYVACTPPSAPQNLININQTTVLSWSPADNGGRNDV 363
DB 330 EEAATSCVCEKDYFRRESDPYVACTPPSAPRANLISNVETSVLEWIPFADTGGRKDV 389
QY 364 TYRILCKRCGMEQCEVPCGSNIGYMPQOTGLEDNVYVMDLLAHANYTFEEVAVNGVSD 423
DB 390 SYTIACKCKNSHAGVCECGHRYLPRQSGLKNTSVMMDLLAHNTYTFIEAVNGVSD 449
QY 424 LSRSORLFAAVSITTTQGAAPSOVSGVWKERVLORSVOLSMQEPHNGVITTEYIKYK 483
DB 450 LSPGARQYVSVNTTQGAAPSPVTNVKKGKIAKNSISLSWQEPDRPNGIILEYIKYFEK 509
QY 484 DQERTYSTLKTSTASINNLKGTYYVFOIRAVTAAGYNSPRLDVATLEASGKMF 543
DB 510 DQ-ETSYTIKSKETITTAGLKPASVYFOIRARTAGYGVFSRPE-----F 557
QY 544 EAT---AVSSEQNPVILIAVAVAGTIIIVMVFGFI-----GRR----- 581

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Db 558 ETPVFAASSDQSOIPVIAVSIVG-VILLAVIGVLLSSGCCGCGRASSLCAVAHPI 616
 QY 582 ---HCGYSKADQEGDEE-LYFHS 600
 Db 617 LWRGYSKAKODPEEKMHFN 639

RESULT 11
 ADE31683
 ID ADE31683 standard; protein; 1037 AA.
 XX ADE31683;
 AC ADE31683;
 DT 29-JAN-2004 (first entry)
 XX
 DE Human 1419 protein #SEQ ID 40.
 XX
 KM Antihypertensive; cardiac; vasodilator; anti-inflammatory;
 KM thrombolytic; antiarrhythmic; antianginal; hypotensive; gene therapy;
 KM cardiovascular disease; ischemia; aortic bending;
 KM vascular heart disease; endocarditis; atrial fibrillation; heart failure;
 KM angina; cardiomyopathy; cardiac death.
 XX
 OS Homo sapiens.
 XX
 PN WO2003065984-A2.
 XX
 PD 14-AUG-2003.
 XX
 PF 29-JAN-2003; 2003WO-US002571.
 XX
 PR 01-FEB-2002; 2002US-0353224P.
 PR 15-MAR-2002; 2002US-0354529P.
 PR 19-APR-2002; 2002US-0373861P.
 PR 29-APR-2002; 2002US-0376287P.
 PR 12-JUN-2002; 2002US-0388080P.
 PR 24-JUN-2002; 2002US-0390971P.
 PR 03-JUL-2002; 2002US-0394130P.
 PR 10-JUL-2002; 2002US-0394797P.
 PR 21-AUG-2002; 2002US-0404904P.
 PR 23-AUG-2002; 2002US-0405450P.
 PR 04-SEP-2002; 2002US-0408070P.
 PR 06-NOV-2002; 2002US-0424300P.
 PR 05-DEC-2002; 2002US-0431042P.
 PR 05-DEC-2002; 2002US-0431079P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Logan TJ, Chun M, Galvin KM, Healy A, Acton SL, Donaghy M;
 PI Scagliano N, Perodin J, Rodrigue-Way A;
 XX
 DR WPI; 2003-731468/69.
 DR N-PSDB; ADE31682.
 XX
 PT Identifying a compound capable of treating a cardiovascular disorder
 PT (e.g. atherosclerosis) comprises assaying the ability of the compound to
 PT modulate the expression or activity of e.g. 1682, 6169 or 6193
 PT polypeptide or nucleic acid.
 XX
 PS Disclosure; SEQ ID NO 40; 328bp; English.
 XX
 CC The invention relates to a method for identifying a compound capable of
 CC treating a cardiovascular disorder. The present invention identifies the
 CC differential expression of 1682, 6169, 6193, 7771, 14395, 29002, 33216,
 CC 43726, 69292, 21656, 32427, 2402, 7747, 1720, 7771, 14395, 29002, 33216,
 CC 33207, 1419, 18036, 16105, 38650, 14245, 58848, 1870, 25856, 33294, 3484,
 CC 345, 9252, 9135, 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912,
 CC 2868, 283, 2854, 9464, 17799, 26686, 43848, 32135, 12208, 2914, 51130,
 CC 19489, 21833, 2517, 59590, 15992, 2094, 2252, 3474, 9792, 15400, 1432 or
 CC 6585 genes in cardiovascular disease states. The methods are useful in
 CC diagnosing, preventing and treating cardiovascular disorders, such as
 CC atherosclerosis, cardiac hypertrophy, ischemia, reperfusion injury,

CC restenosis, arterial inflammation, vascular wall remodeling, coronary
 CC microembolism, tachycardia, bradycardia, pressure overload, aortic
 CC bending, coronary artery ligation, vascular heart disease, valvular
 CC disease, including but not limited to, valvular degeneration caused by
 CC calcification, rheumatic heart disease, endocarditis, or complications of
 CC artificial valves; atrial fibrillation, long-QT syndrome, congestive
 CC heart failure, sinus node dysfunction, angina, heart failure,
 CC hypertension, atrial fibrillation, atrial flutter, pericardial disease,
 CC including but not limited to, pericardial effusion and pericarditis;
 CC cardiomyopathies, e.g. dilated cardiomyopathy or idiopathic
 CC cardiomyopathy, myocardial infarction, coronary artery disease, coronary
 CC artery spasm, ischemic disease, arrhythmia, sudden cardiac death and
 CC cardiovascular developmental disorders. The methods may also be used for
 CC identifying compounds that modulate cardiovascular disorders. Sequences
 CC given in ADE31644-ADE31769 represent the genes and proteins that may be
 CC regulated by a compound of the invention.
 CC
 XX
 S0 Sequence 1037 AA;
 Query Match 54.4%; Score 1817; DB 7; Length 1037;
 Best Local Similarity 55.5%; Pred. No. 2.1e-152;
 Matches 346; Conservative 97; Mismatches 132; Indels 48; Gaps 10;
 QY 6 RFPSSW--IILCYIWLGFHATGEAQAKEYLLDSKAQOTELEWISSPPSGWERISGIDE 63
 Db 37 RAPIMTCLLLC-----AALRTLLASPSNEVNLDSRTVMGDLGIAPKNGMEIGEVDE 91
 QY 64 NYTPFRTYQVCQWEPNQNMLRTNWSKGNARIFVELKFTLBDNLSLPGVLTCKETP 123
 Db 92 NYAPIHITYQVCKWEOQNMMWLLTSMISNEGASRIFTELFTLRDCCNSLPGGLTCKETP 151
 QY 124 NLVYFETDPTDGNIRNLYVVKIDITLADSEFTQGDGGERKMKLNTVREIGPLSKGIFY 183
 Db 152 NMYTFESDDQNGRNKIKNOYIKIDITLADSEFTLGDGMKLNTRYRIVGPKSKGIFY 211
 QY 184 LAFQDVACIALVSVKYYKCKWTIVENLAVFPDPTVTSSEFSSILVEVGTQVSAEEBAE 243
 Db 212 LAFQDVACIALVSVRYKKCPSVVHLAVFPDPTVIGADSSQLLEVSQSVN--HSVTD 269
 QY 244 NSPMHGSAGSEMLVPIGKICRAGYQKQKDTCEPCRRYKSSQLQSRCTHPSFD 303
 Db 270 EPPMHGSAGSEMLVPIGKICRAGYEKNKGTQVCPGPFKASPHIQSGCKEPPHSYTH 329
 QY 304 REGSSRCEGDEGYRAPSPPVACTRPPAPONLIFINQTTVSLKSPADNCGRNDV 363
 Db 330 EEAISTCVCEKDFRRESPPYMACTRPPAPRAVLSNVETSVFLMIPADTGCKDV 389
 QY 364 TYRILCRCSMEQECVPCGSGNIGYMPQOTGLEDDNYTVMDLAAHANYTEVEAVNGVSD 423
 Db 390 SYTIACKCKSHAGVCECGGHRVYLPROSGLNKTSMMVMDLAHTMYTEIEIAVNGVSD 449
 QY 424 LRSQRLPAVSTTGOAPSOVSGVKEKERVLSVOLSQOEPHNGVITEIKIYK 483
 Db 450 LSPGARQYVSVNVTNQAAPSPVNTVKKRIAKNSISLSQOEPDRPGIILEYIKHFEK 509
 QY 484 DQERTSTLKTSTASINNLKRGTYVVOIRAVTAAGVNSPRDVAATLEASGMF 543
 Db 510 DQ-STSTIITKSTETTAAGLKPASVYVQIRARTAGVGVSRPE-----F 557
 QY 544 EAT---AVSEHONPVIIVAAVAGTIIIVFMVFGFI-----GRR----- 581
 Db 558 ETPVFAASSDQSOIPVIAVSIVG-VILLAVIGVLLSSGCCGCGRASSLCAVAHPI 616
 QY 582 ---HCGYSKADQEGDEE-LYFHS 600
 Db 617 LWRGYSKAKODPEEKMHFN 639

RESULT 12
 ABP52827
 ID ABP52827 standard; protein; 975 AA.
 AC ABP52827;

| Result No. | Score | Query Length | DB | ID | Description |
|------------|--------|--------------|------|----|---------------------|
| 1 | 3242 | 100.0 | 610 | 2 | developmental kina |
| 2 | 3203.5 | 98.8 | 605 | 2 | receptor tyrosine |
| 3 | 3199 | 98.6 | 626 | 2 | developmental kina |
| 4 | 3191 | 98.4 | 998 | 2 | receptor tyrosine |
| 5 | 3139 | 96.8 | 998 | 2 | receptor protein-t |
| 6 | 1843 | 56.8 | 991 | 2 | receptor protein-t |
| 7 | 1836 | 56.6 | 981 | 2 | receptor-like tyro |
| 8 | 1821 | 56.2 | 1005 | 2 | receptor tyrosine |
| 9 | 1802 | 55.6 | 1013 | 2 | receptor-type prot |
| 10 | 1799 | 55.5 | 983 | 2 | receptor tyrosine k |
| 11 | 1789.5 | 55.1 | 985 | 2 | receptor tyrosine |
| 12 | 1786.5 | 55.1 | 983 | 2 | receptor tyrosine |
| 13 | 1786.5 | 55.1 | 983 | 2 | receptor tyrosine |
| 14 | 1736.5 | 53.5 | 986 | 2 | receptor protein-t |
| 15 | 1718 | 53.0 | 986 | 2 | protein-tyrosine k |
| 16 | 1662 | 51.2 | 948 | 2 | receptor-like tyro |
| 17 | 1500.5 | 46.3 | 995 | 2 | embryo kinase 5 - |
| 18 | 1470 | 45.3 | 970 | 2 | receptor protein-t |
| 19 | 1449 | 44.2 | 984 | 2 | protein-tyrosine k |
| 20 | 1400 | 43.2 | 988 | 2 | receptor tyrosine |
| 21 | 1392 | 42.9 | 893 | 2 | receptor-like tyro |
| 22 | 1348 | 41.6 | 985 | 2 | receptor tyrosine |
| 23 | 1330 | 41.0 | 849 | 2 | protein-tyrosine k |
| 24 | 1276 | 39.3 | 988 | 2 | protein-tyrosine k |
| 25 | 1271 | 39.2 | 998 | 2 | protein-tyrosine k |
| 26 | 1269.5 | 39.1 | 992 | 2 | mouse developmenta |
| 27 | 1253.5 | 38.7 | 992 | 2 | protein-tyrosine k |
| 28 | 1248.5 | 38.0 | 976 | 2 | protein-tyrosine k |
| 29 | 1233.5 | 38.5 | 877 | 2 | brain-specific kin |

| | | | | | | |
|----|--------|------|------|---|--------|--------------------|
| 30 | 1139.5 | 37.0 | 977 | 2 | S49074 | protein kinase Mpk |
| 31 | 1166.5 | 36.0 | 938 | 2 | I49071 | protein kinase - m |
| 32 | 1139.5 | 35.1 | 975 | 2 | I48974 | receptor-protein t |
| 33 | 1072.5 | 33.1 | 1006 | 2 | JC5526 | kinase-defective E |
| 34 | 1064.5 | 32.8 | 984 | 1 | A34076 | protein-tyrosine k |
| 35 | 1035.5 | 31.9 | 987 | 2 | I48652 | mouse developmenta |
| 36 | 1034 | 31.9 | 987 | 2 | A54092 | protein-tyrosine k |
| 37 | 1022.5 | 31.5 | 987 | 2 | I48953 | eph-related recept |
| 38 | 784 | 24.2 | 1019 | 2 | T13039 | tyrosine kinase re |
| 39 | 544 | 16.8 | 1122 | 2 | T42400 | Eph receptor tyros |
| 40 | 382.5 | 11.8 | 919 | 2 | T29581 | hypothetical prote |
| 41 | 362 | 11.2 | 612 | 2 | S33506 | protein-tyrosine k |
| 42 | 251 | 7.7 | 87 | 2 | C45583 | receptor tyrosine |
| 43 | 215.5 | 6.6 | 1232 | 2 | T43027 | neural cell adhesi |
| 44 | 209 | 6.4 | 1436 | 2 | JC5290 | protein-tyrosine-p |
| 45 | 206.5 | 6.4 | 1855 | 2 | C88400 | protein H19M22.1 (|

ALIGNMENTS

RESULT 1

developmental kinase 1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I48612; S51741
R:Ciossek, T.; Millauer, B.; Ullrich, A.
Oncogene 9, 97-108, 1995
A:Title: Identification of alternatively spliced mRNA encoding variants of MDK1, a novel
A:Reference number: I48611
A:Accession: I48612
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule_type: mRNA
A:Residues: 1-610 <RES>
A:Cross-references: UNIPROT:Q61772; EMBL:X79083; NID:5607135; PIDN:CA55688.1; PID:5607135

| | | | | |
|-------------|---------|-------------|-------|------------|
| Query Match | 100.0%; | Score 3243; | DB 2; | Length 610 |
|-------------|---------|-------------|-------|------------|

Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| Qy | 1 | MMVQTFPSPMIIICVIMLLGFANHTBAQAALVLLMSKAQTELEWISSPSSGMEISG | 60 |
| Db | 1 | MMVQTFPSPMIIICVIMLLGFANHTBAQAALVLLMSKAQTELEWISSPSSGMEISG | 60 |
| Qy | 61 | LDENYTPIRITTYOVCOVMEPNONNMWRITWISKGNARIFVELKTTLRDCNSLPSVJGTC | 120 |
| Db | 61 | LDENYTPIRITTYOVCOVMEPNONNMWRITWISKGNARIFVELKTTLRDCNSLPSVJGTC | 120 |
| Qy | 121 | ETFNLYYYEDVDYDGTGNIRENLYVKIDITIADESTQGDJGERMKKNTREVRIGPLSKK | 180 |
| Db | 121 | ETFNLYYYEDVDYDGTGNIRENLYVKIDITIADESTQGDJGERMKKNTREVRIGPLSKK | 180 |
| Qy | 181 | GFYIAFQDYAGACIALSVSVYKXKCMTIVENLAVFPDITVTSSEFSSLVEVNGTCSAAE | 240 |
| Db | 181 | GFYIAFQDYAGACIALSVSVYKXKCMTIVENLAVFPDITVTSSEFSSLVEVNGTCSAAE | 240 |
| Qy | 241 | EAENSFRMHCSABGEMLVPIGKCTICAGYQOKGDTCEPCGRRFRYKSSQDILQSCRCTHS | 300 |
| Db | 241 | EAENSFRMHCSABGEMLVPIGKCTICAGYQOKGDTCEPCGRRFRYKSSQDILQSCRCTHS | 300 |
| Qy | 301 | FSDRESSRSCBCEGDGYRAPSDPPVYACRPSAPQNLIPINQTTVSLSEMSPADNGGR | 360 |
| Db | 301 | FSDRESSRSCBCEGDGYRAPSDPPVYACRPSAPQNLIPINQTTVSLSEMSPADNGGR | 360 |
| Qy | 361 | NDVTYRILICRSCMEGECVPCGSNIGYMPQDTGLENDYVTYMDLLAHANTFEVEAVNG | 420 |
| Db | 361 | NDVTYRILICRSCMEGECVPCGSNIGYMPQDTGLENDYVTYMDLLAHANTFEVEAVNG | 420 |
| Qy | 421 | VSLSRSSQSLFPAVASTITGQAAPSOVSGYMKERVQBSVOLSMQEPHPNVCVITREYIKY | 480 |
| Db | 421 | VSLSRSSQSLFPAVASTITGQAAPSOVSGYMKERVQBSVOLSMQEPHPNVCVITREYIKY | 480 |

QY 481 YEKDQERRTYSLTKTSTASINNLKPGTVYVFOIRAVTAAGYNSPRLDVATLEBASG 540
 |||
 Db 481 YEKDQERRTYSLTKTSTASINNLKPGTVYVFOIRAVTAAGYNSPRLDVATLEBASG 540
 |||
 QY 541 KMEFATVASEQNPVILIAVAVAGTILVFWFGFIIIGRRHCGYSKADQEGDEELYFHS 600
 |||
 Db 541 KMEFATVASEQNPVILIAVAVAGTILVFWFGFIIIGRRHCGYSKADQEGDEELYFHS 600
 |||
 QY 601 LVTNEHLSVL 610
 |||
 Db 601 LVTNEHLSVL 610
 |||

RESULT 2

JC5673
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Nov-1997 #sequence_revision 20-Nov-1997 #text_change 07-May-1999
 C:Accession: JC5673
 R:Author: A.H.; Muramatsu, T.; Kaneda, N.
 R:Title: A novel truncated variant form of Etk/MDK1 receptor tyrosine kinase is expressed
 A:Reference number: JC5672; MUID:98035156; PMID:9368721
 A:Accession: JC5673
 A:Molecule type: mRNA
 A:Residues: 1-605 <TAL>
 A:Experimental source: embryo
 C:Comment: This enzyme plays a regulatory role during neural development and embryogenesis
 C:Keywords: brain; phosphotransferase
 F:1-30/Domain: signal sequence #status predicted <SIG>
 F:31-605/Product: receptor tyrosine kinase Etk-ctd1 #status predicted <MAT>
 F:31-548/Domain: extracellular #status predicted <EXT>
 F:311-438/Domain: fibronectin type III repeat <FN3>
 F:441-534/Domain: fibronectin type III repeat <FN2>
 F:549-574/Domain: transmembrane #status predicted <TM>

Query Match 98.8%; Score 3203.5; DB 2; Length 605;
 Best Local Similarity 99.2%; Pred. No. 8.3e-224;
 Matches 605; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 MVVQTRPSPWIIICYLWLGFAHTGEAOAKEVLLDLSKAQOTELEWISSPPSGMEISG 60
 |||
 Db 1 MVVQTRPSPWIIICYLWLGFAHTGEAOAKEVLLDLSKAQOTELEWISSPPSGMEISG 60
 |||
 QY 61 LDENYPIRTYQVCQWEPNQNMLRTNWSKGNARIFVELKFTLRDCNSLPGLVGTCK 120
 |||
 Db 61 LDENYPIRTYQVCQWEPNQNMLRTNWSKGNARIFVELKFTLRDCNSLPGLVGTCK 120
 |||
 QY 121 EFTNLYYETDYGNGIRNENLVKIDTIAADSFQSGDGERKMKLNTVEIREIGPLSKK 180
 |||
 Db 121 EFTNLYYETDYGNGIRNENLVKIDTIAADSFQSGDGERKMKLNTVEIREIGPLSKK 180
 |||
 QY 181 GFPLAFQDVACIALVSVKYYKKCWTIVENLAVFPDVTGSEFSSLVEVRGCVSSAE 240
 |||
 Db 181 GFPLAFQDVACIALVSVKYYKKCWTIVENLAVFPDVTGSEFSSLVEVRGCVSSAE 240
 |||
 QY 241 EAENSFRMHCASAGEWLVPIGKICRAGYQOKGDTCEPCGRFRYKSSODLQCSRCPTHS 300
 |||
 Db 241 EAENSFRMHCASAGEWLVPIGKICRAGYQOKGDTCEPCGRFRYKSSODLQCSRCPTHS 300
 |||
 QY 301 FSDREGSSRCCECDGYRASPDPYVACTRPPSAPNLFNINQTVSLFMSPPADNGR 360
 |||
 Db 301 FSDREGSSRCCECDGYRASPDPYVACTRPPSAPNLFNINQTVSLFMSPPADNGR 360
 |||
 QY 361 NDVTYRILCKRCMEQGEVPCGSNIGVMPQOTGLENDYVWMDLAHANYTEVEAVNG 420
 |||
 Db 361 NDVTYRILCKRCMEQGEVPCGSNIGVMPQOTGLENDYVWMDLAHANYTEVEAVNG 420
 |||
 QY 421 VSDLSRSQRLFAVASTTGOAAPSQVSGWKERVLRQSVLSQDEPHNGVITTEYIKY 480
 |||
 Db 421 VSDLSRSQRLFAVASTTGOAAPSQVSGWKERVLRQSVLSQDEPHNGVITTEYIKY 480
 |||
 QY 481 YEKDQERRTYSLTKTSTASINNLKPGTVYVFOIRAVTAAGYNSPRLDVATLEBASG 540
 |||

Db 481 YEKDQERRTYSLTKTSTASINNLKPGTVYVFOIRAVTAAGYNSPRLDVATLEBAS- 539
 |||
 QY 541 KMEFATVASEQNPVILIAVAVAGTILVFWFGFIIIGRRHCGYSKADQEGDEELYFHS 600
 |||
 Db 540 ----ATVASEQNPVILIAVAVAGTILVFWFGFIIIGRRHCGYSKADQEGDEELYFHS 595
 |||
 QY 601 LVTNEHLSVL 610
 |||
 Db 596 LVTNEHLSVL 605
 |||

RESULT 3

I48614
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C:Accession: I48614; S51742
 R:Author: T.; Miliuter, B.; Ullrich, A.
 R:Title: Identification of alternatively spliced mRNA encoding variants of MDK1, a novel
 A:Reference number: I48611
 A:Accession: I48614
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-626 <RES>
 A:Cross-references: UNIPROT:Q61772; EMBL:X79084; NID:G607137; PID:CAA55689.1; PID:G60713;

Query Match 98.6%; Score 3199; DB 2; Length 626;
 Best Local Similarity 100.0%; Pred. No. 1.8e-223;
 Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVVQTRPSPWIIICYLWLGFAHTGEAOAKEVLLDLSKAQOTELEWISSPPSGMEISG 60
 |||
 Db 1 MVVQTRPSPWIIICYLWLGFAHTGEAOAKEVLLDLSKAQOTELEWISSPPSGMEISG 60
 |||
 QY 61 LDENYPIRTYQVCQWEPNQNMLRTNWSKGNARIFVELKFTLRDCNSLPGLVGTCK 120
 |||
 Db 61 LDENYPIRTYQVCQWEPNQNMLRTNWSKGNARIFVELKFTLRDCNSLPGLVGTCK 120
 |||
 QY 121 EFTNLYYETDYGNGIRNENLVKIDTIAADSFQSGDGERKMKLNTVEIREIGPLSKK 180
 |||
 Db 121 EFTNLYYETDYGNGIRNENLVKIDTIAADSFQSGDGERKMKLNTVEIREIGPLSKK 180
 |||
 QY 181 GFPLAFQDVACIALVSVKYYKKCWTIVENLAVFPDVTGSEFSSLVEVRGCVSSAE 240
 |||
 Db 181 GFPLAFQDVACIALVSVKYYKKCWTIVENLAVFPDVTGSEFSSLVEVRGCVSSAE 240
 |||
 QY 241 EAENSFRMHCASAGEWLVPIGKICRAGYQOKGDTCEPCGRFRYKSSODLQCSRCPTHS 300
 |||
 Db 241 EAENSFRMHCASAGEWLVPIGKICRAGYQOKGDTCEPCGRFRYKSSODLQCSRCPTHS 300
 |||
 QY 301 FSDREGSSRCCECDGYRASPDPYVACTRPPSAPNLFNINQTVSLFMSPPADNGR 360
 |||
 Db 301 FSDREGSSRCCECDGYRASPDPYVACTRPPSAPNLFNINQTVSLFMSPPADNGR 360
 |||
 QY 361 NDVTYRILCKRCMEQGEVPCGSNIGVMPQOTGLENDYVWMDLAHANYTEVEAVNG 420
 |||
 Db 361 NDVTYRILCKRCMEQGEVPCGSNIGVMPQOTGLENDYVWMDLAHANYTEVEAVNG 420
 |||
 QY 421 VSDLSRSQRLFAVASTTGOAAPSQVSGWKERVLRQSVLSQDEPHNGVITTEYIKY 480
 |||
 Db 421 VSDLSRSQRLFAVASTTGOAAPSQVSGWKERVLRQSVLSQDEPHNGVITTEYIKY 480
 |||
 QY 481 YEKDQERRTYSLTKTSTASINNLKPGTVYVFOIRAVTAAGYNSPRLDVATLEBASG 540
 |||
 Db 481 YEKDQERRTYSLTKTSTASINNLKPGTVYVFOIRAVTAAGYNSPRLDVATLEBASG 540
 |||
 QY 541 KMEFATVASEQNPVILIAVAVAGTILVFWFGFIIIGRRHCGYSKADQEGDEELYFHS 600
 |||
 Db 541 KMEFATVASEQNPVILIAVAVAGTILVFWFGFIIIGRRHCGYSKADQEGDEELYFHS 600
 |||
 QY 601 L 601

Db 601 L 601

RESULT 4

JC5672 receptor tyrosine kinase (EC 2.7.-.-) Etk precursor - mouse

N:Alternate names: developmental kinase 1

C/Species: Mus musculus (house mouse)

C/Date: 20-Nov-1997 #sequence revision 20-Nov-1997 #text_change 09-Jul-2004

C/Accession: JC5672; I48611; S51740

R:Translator: A.H.; Muramatsu, T.; Kaneda, N.

Cell Struct. Funct. 22, 477-485, 1997

A>Title: A novel truncated variant form of Etk/MDK1 receptor tyrosine kinase is expressed

A/Reference number: JC5672; MUID:98035156; PMID:9368721

A/Accession: JC5672

A/Molecule type: mRNA

A/Residues: 1-998 <TAL>

A/Cross-references: UNIPROT:Q61772

A/Experimental source: embryo

R/Closter, T.; Millauer, B.; Ullrich, A.

Oncogene 9, 97-108, 1995

A>Title: Identification of alternatively spliced mRNA encoding variants of MDK1, a novel

A/Reference number: I48611

A/Accession: I48611

A/Molecule type: translated from GB/EMBL/DBJ

A/Status: preliminary

A/Residues: 1-998 <RES>

A/Cross-references: EMBL:X79082; NID:9607133; PIDN:CAA55687.1; PID:9607134

C/Comment: This enzyme plays a role during development involving differentiation and pro

C/Superfamily: protein-tyrosine kinase, receptor type eph, fibronectin type III repeat h

C/Keywords: ATP; brain; phosphotransferase; transmembrane protein

F:1-30/Domain: signal sequence #status predicted <SIG>

F:31-998/Product: receptor tyrosine kinase Etk #status predicted <MAT>

F:31-553/Domain: extracellular #status predicted <EXT>

F:331-438/Domain: fibronectin type III repeat <FN1>

F:441-534/Domain: fibronectin type III repeat <FN2>

F:554-579/Domain: transmembrane #status predicted <TM>

F:631-697/Domain: protein kinase homology <KIN>

F:639-647/Region: protein kinase ATP-binding motif

F:920-986/Domain: SAM homology <SAM>

Query Match 98.4%; Score 3191; DB 2; Length 998;

Best Local Similarity 100.0%; Pred. No. 1.3e-222;

Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTQTRPSPWIIICYLWLGFAHTGEAQAKEVLLDSKAQOTLEWISSPPSGMEETISG 60

DB 1 MVTQTRPSPWIIICYLWLGFAHTGEAQAKEVLLDSKAQOTLEWISSPPSGMEETISG 60

QY 61 LDEYVTPIRTYQVQVWEPNWNMLRTNWSKGAQRIFVELKFTLDQNSLPVLTGTC 120

DB 61 LDEYVTPIRTYQVQVWEPNWNMLRTNWSKGAQRIFVELKFTLDQNSLPVLTGTC 120

QY 121 ETEFLYYETDYPDGRNIRENLVYKIDTIADESFTQGDGERKMKLNTVEIREIGPLSK 180

DB 121 ETEFLYYETDYPDGRNIRENLVYKIDTIADESFTQGDGERKMKLNTVEIREIGPLSK 180

QY 181 GFYLAPODVAGACIALVSVKYYKKCWITVENLAVFPDVTGSESSSLVEVRGTCVSSAE 240

DB 181 GFYLAPODVAGACIALVSVKYYKKCWITVENLAVFPDVTGSESSSLVEVRGTCVSSAE 240

QY 241 EAENSPPMHCSABEEMLVPIGKCI CKAGYQOKGDTCEPCGRRPFKSSSODLQSCRCPHS 300

DB 241 EAENSPPMHCSABEEMLVPIGKCI CKAGYQOKGDTCEPCGRRPFKSSSODLQSCRCPHS 300

QY 301 FSDREGSSRCCEGEGYRAPSDPYVACTRPPSAPOULIFININOTVLSLEMSPPADNGR 360

DB 301 FSDREGSSRCCEGEGYRAPSDPYVACTRPPSAPOULIFININOTVLSLEMSPPADNGR 360

QY 361 NDVTYRILCKRCSWEGECVPCGSNIGYMPQOTGLEBNYTVMDLAAHYATTFEVAANG 420

DB 361 NDVTYRILCKRCSWEGECVPCGSNIGYMPQOTGLEBNYTVMDLAAHYATTFEVAANG 420

QY 421 VSDLSRSQRLFAAVSITTTGAAPSQVSGWKERVLRQSVOLSWQEPHPNGVITEYIKY 480

DB 421 VSDLSRSQRLFAAVSITTTGAAPSQVSGWKERVLRQSVOLSWQEPHPNGVITEYIKY 480

QY 481 YEKQRRERTYSTLTKTSASINLTKPGTYVVPQIRAVTAAGYGNVSPRLDVALLEBASG 540

DB 481 YEKQRRERTYSTLTKTSASINLTKPGTYVVPQIRAVTAAGYGNVSPRLDVALLEBASG 540

QY 541 KMFETAVSSBONPVIIIAVAVAGTIIIVFMVGFIIGRHCGYSKADQDEBELYFH 599

DB 541 KMFETAVSSBONPVIIIAVAVAGTIIIVFMVGFIIGRHCGYSKADQDEBELYFH 599

RESULT 5

158351 receptor protein-tyrosine kinase - human

C/Species: Homo sapiens (man)

C/Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text_change 09-Jul-2004

C/Accession: 158351

R/Fox, G.M.; Holst, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu, R.; Welcher,

Oncogene 10, 897-905, 1995

A>Title: cDNA cloning and tissue distribution of five human EPH-like receptor protein-ty-

A/Reference number: 158351; MUID:95206782; PMID:7898931

A/Accession: 158351

A/Status: preliminary

A/Molecule type: translated from GB/EMBL/DBJ

A/Residues: 1-998 <RES>

A/Cross-references: UNIPROT:Q15375; GB:J36642; NID:9551607; PIDN:AAA74243.1; PID:9551608

C/Genetics:

C/Superfamily: protein-tyrosine kinase, receptor type eph, fibronectin type III repeat h

C/Keywords: ATP; transmembrane protein

F:631-697/Domain: protein kinase homology <KIN>

F:639-647/Region: protein kinase ATP-binding motif

F:920-986/Domain: SAM homology <SAM>

Query Match 96.8%; Score 3139; DB 2; Length 998;

Best Local Similarity 97.7%; Pred. No. 7.5e-219;

Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

QY 1 MVTQTRPSPWIIICYLWLGFAHTGEAQAKEVLLDSKAQOTLEWISSPPSGMEETISG 60

DB 1 MVTQTRPSPWIIICYLWLGFAHTGEAQAKEVLLDSKAQOTLEWISSPPSGMEETISG 60

QY 61 LDEYVTPIRTYQVQVWEPNWNMLRTNWSKGAQRIFVELKFTLDQNSLPVLTGTC 120

DB 61 LDEYVTPIRTYQVQVWEPNWNMLRTNWSKGAQRIFVELKFTLDQNSLPVLTGTC 120

QY 121 ETEFLYYETDYPDGRNIRENLVYKIDTIADESFTQGDGERKMKLNTVEIREIGPLSK 180

DB 121 ETEFLYYETDYPDGRNIRENLVYKIDTIADESFTQGDGERKMKLNTVEIREIGPLSK 180

QY 181 GFYLAPODVAGACIALVSVKYYKKCWITVENLAVFPDVTGSESSSLVEVRGTCVSSAE 240

DB 181 GFYLAPODVAGACIALVSVKYYKKCWITVENLAVFPDVTGSESSSLVEVRGTCVSSAE 240

QY 241 EAENSPPMHCSABEEMLVPIGKCI CKAGYQOKGDTCEPCGRRPFKSSSODLQSCRCPHS 300

DB 241 EAENSPPMHCSABEEMLVPIGKCI CKAGYQOKGDTCEPCGRRPFKSSSODLQSCRCPHS 300

QY 301 FSDREGSSRCCEGEGYRAPSDPYVACTRPPSAPOULIFININOTVLSLEMSPPADNGR 360

DB 301 FSDREGSSRCCEGEGYRAPSDPYVACTRPPSAPOULIFININOTVLSLEMSPPADNGR 360

QY 361 NDVTYRILCKRCSWEGECVPCGSNIGYMPQOTGLEBNYTVMDLAAHYATTFEVAANG 420

DB 361 NDVTYRILCKRCSWEGECVPCGSNIGYMPQOTGLEBNYTVMDLAAHYATTFEVAANG 420

QY 421 VSDLSRSQRLFAAVSITTTGAAPSQVSGWKERVLRQSVOLSWQEPHPNGVITEYIKY 480

DB 421 VSDLSRSQRLFAAVSITTTGAAPSQVSGWKERVLRQSVOLSWQEPHPNGVITEYIKY 480


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Oy      481  YEKQREHYTTLTKKTSASINLKGQYVVFQIRAVTAYGNYSPRLDVALEASG 540
      :|
Db      481  YEKQREHYTIVTKTSASINLKGQYVVFQIRAVTAYGNYSPRLDVALEASG 540

Oy      541  KMFATAVSSQNPVLIIVAVVAGTIIILVFMVFGFIIGRRHCYSGADQEGDELYFH 599
      541  KMFATAVSSQNPVLIIVAVVAGTIIILVFMVFGFIIGRRHCYSGADQEGDELYFH 599

RESULT 6
178843  receptor protein-tyrosine kinase - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 18-Jun-1999
C/Accession: 178843
R/Fox, G.M.; Holst, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu, R.; Welcher,
Oncogene 10, 897-905, 1995
A/Title: cDNA cloning and tissue distribution of five human EPH-like receptor protein-ty
A/Reference number: 158351; MUID:95206782; PMID:7898931
A/Accession: 178843
A/Status: preliminary; translated from GB/EMBL/DBD
A/Molecule type: mRNA
A/Residues: 1-991 <RSS>
A/Cross-references: GB:IJ6644; NID:G551611; PIDN:AAA74245.1; PID:G551612
C/Genetics:
A/Gene: HEKY
C/Superfamily: protein-tyrosine kinase, receptor type eph, fibronectin type III repeat h
E/627-893/Domains: protein kinase homology <KIN>
E/916-982/Domains: SAM homology <SAM>

```

```

OY      600 SLVTNEHLSV 609
      | | :
Db      593 ----NGHIKL 598

RESULT 7
S51604
receptor-like tyrosine kinase Etk-1 - rat
C|Species: Rattus norvegicus (Norway rat)
C|Date: 07-May-1995 #sequence_revision 21
C|Accession: S51604
R|Maisompierre, P.C.; Barrezueta, N.X.; Yancopoulos, G.D.
Oncogene 8, 3277-3288, 1993
A|Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase fam
A|Reference number: S49015; MUID:94067777; PMID:7504232
A|Accession: S51604
A|Status: preliminary
A|Molecule type: mRNA
A|Residues: 1-981 <MAI>
A|Cross-references: EMBL:S68029
A|Note: the authors translated the codon GAC for residue 170 as Glu
C|Superfamily: protein-tyrosine kinase, receptor type epi, fibronectin type III repeat ho
C|Keywords: ATP, transmembrane protein
P:651-917/Domain: protein kinase homology <KIN>
P:653-667/Region: protein kinase ATP-binding motif

```

Query March 56.9% Score 1843; DB 2; Length 991;
Best Local Similarity 56.9%; Pred. No. 4,1e-125;
Matches 347; Conservative 98; Mismatches 15; Indels 30; Gaps 9;

```
QY      6 RPSWM--IIICYLWLGFAHTGEAQAKEVILLDSKAQOLETELWISSPPSGMEIISGLDE 63
Db      13 RAPMTCLILC-----AALRTILASPSENEVILLDSRTVMGLGIWAIPKNGMEIIGVE 67

QY      64 NYTPIRITYOVONWEPNONMRLRTNWI SKGAQRI FPEIKETLLADCSLPGVGTCKETF 123
Db      68 NYAIPHIYQVCKWEQONMNLTSWISNEGASRI FLEKFTLLDCNSLPGGLGTCKETF 127

QY      124 NLVYETDYDGRNIRENLVYKIDITLADSEFTGGDGERKMKNTREIREIGPLSKKGFY 183
Db      128 NMYIFESDDQGRNIKENQYIKIDITLADSEFTLELDGDRMKNTREVRVGPISKKGFY 187

QY      184 LAPDVGACIALVSVKYYKKCCMTIVENLAVPDTVTGSEBSLVEYRGTCVSSAEAEAE 243
Db      188 LAPDVGACIALVSVRYKKCPSVRHLLAVFPDTITGADSSQLLEVSGSCVN--HSVTD 245

QY      244 NSPRMHGSAEGEWLVPIGKCI CKAGYOOKGDTGCPGRRPFKSSQDLOCRCRTHFS 303
Db      246 EPPMHGSAEBEMLVPIGKCMCKAGYEKNGTCVCCPGRFFKASPHIQSGCKCPHSYTH 305

QY      304 REGSSRCECEDGYRAPSDPPTYVACTRPPAPQNLININOTIVSLEMSPEADNGRNDV 363
Db      306 EEASTSCYCEKDXPRRSDPPTYMACTRPPAPRAVISNVAIETSVFLEMIIPADIGKRDV 365

QY      364 TYRLCKRCSEGEQECPCPGSNIGMPQOQTELENNYTTWMDLHANATTEVEAVNGSD 423
Db      366 SYTLACKKCNHSAVCEEGGHVRYLLPQSLKNTKTSVMVDLLAHATYTEIEIEVNGSD 425

QY      424 LSRQSLFLFAVSIITGQAPAPSOVGVNKKERYLQRPVOLSQMOEPHNGVTEYEIKTYEK 483
Db      426 LSPGARQVSVNVTNNQAPSPVTVNKKGKGLAKSISLSQMOEPHNGIILLEYIKRIFEK 485

QY      484 DQRERTSYLTKTKSTASINNLKPGTVYVFOIRAVTAAGYGNVSPRLDVAITBEASGMP 543
Db      486 DQ-ETSYTIIKSKETTTIAGELKPASVYFOIRARTAGGVGFSSRRRE-----F 533

QY      544 EAT---AVSSKQNVIIIAVAVAVAGTIIIVMGVGIIGRRHCGSKADEGDEE-LYFH 599
Db      534 ETTVEFAASQSOQIPIVAIVSVTG-VILLAVVIGVLLSGRCGYSIAKDCPBEKKNHFH 592
```

[illegible]

Db 608 PEEBKMHFH---NGHKL 622

RESULT 8

receptor tyrosine kinase Etk-1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
A:Accession: S49015; S51602
R:Miscellaneous: P.C.; Barrezaeta, N.X.; Yancopoulos, G.D.
Oncogene 8, 3277-3288, 1993
A:Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase fam
A:Reference number: S49015; MUID:94067777; PMID:7504232
A:Accession: S49015
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1005 <MA1>
A:Cross-references: UNIPROT:P54757; EMBL:S68024
A:Note: the authors translated the codon GAC for residue 170 as Glu
A:Accession: S51602
A:Molecule type: mRNA
A:Residues: 1-305, 'G', 359-1005 <MA2>
A:Cross-references: EMBL:S68026
A:Note: the authors translated the codon GAC for residue 170 as Glu
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C:Keywords: ATP; transmembrane protein
P:675-941/Domain: protein kinase homology <KIN>
P:683-691/Region: protein kinase ATP-binding motif

Query Match 56.2%; Score 1821; DB 2; Length 1005;
Best Local Similarity 54.6%; Pred. No. 1.6e-123;
Matches 350; Conservative 97; Mismatches 138; Indels 56; Gaps 11;

QY 6 RFEWITLCY-----IW----LLGPAHTGEAQAKEVLLDSKAQTELEWISSPPSG 54
DB 25 RVPASLAKGVSAPLKGPLMTCLLCAALRTLLASPSNEVNLDRVTVGIDGWLAFPNNG 84
QY 55 WEETSGDENTPIRTYOVQVMEPNQNMRLTNWISKGNQRIFVELKFTLRDQNSLPG 114
DB 85 WEETGEVDENAPLHTYOVQVMEQONQNMRLTWSISMEGASRLFTLEKFTLRDQNSLPG 144
QY 115 VLGTCKETFLNYEYETDYDTRNIRENLVYKIDTIADESFTQDGLGRKKKLTVEAREI 174
DB 145 GLGTCKETFLNMYEYSDDENRNKIDNYIKIDTIADESFTLEDGLGRVKKLTVEARDV 204
QY 175 GPLSKGFFYLAFOVGAICALVSVKYYKKCWTIVENLAVFPDPTVTSSEFSSLVEVRGTC 234
DB 205 GPLSKGFFYLAFOVGAICALVSVVYKKCPVVRHLAVFPDPTITGADSSQLLEVSQCS 264
QY 235 VSSAEAEANSPRMHCAEGEWLVPIGCKICAGYQOKGDTCEPCGRFRFYSSQDLOCS 294
DB 265 VN--HSVTDDPKMHCAGEEMLVPIGCKCKAGYEEKNGTCQVCRPFQFASHSQTC 322
QY 295 RCPHTSFDEGSSRCCEGDYVAPSDPVPVACTRPPSPAPQNLIFINQTVLSLEWSP 354
DB 323 KCPHSTHTEBASISVCYCKDYPRESDEPTMACTRPSAPRNALISVNEISVLEWIP 382
QY 355 ADNGRNDVYRIILCKRCSEWQECVPCGSNIGYMPQGTGLDNYVTVMILLAHANTFE 414
DB 383 ADTGCGADVSYIILCKCKNSHAGVCEEGCHVRYLPQOIGLKNISVMMADLATTNTFE 442
QY 415 VEANGVSDLSRSORLFAVYSITGGAAPSOVSGVMEKERVLRVSQVLSMOEHPNVT 474
DB 443 IEANGVSDLSPGTRQYVAVVNTNQAAPSPVTVKGLAKNSISLSWQSPDPNGITL 502
QY 475 EYEIKYEQDERTYTLTKTSASINLKPQVTVVFOIRAYTAAGYGYSPRLDVA 534
DB 503 EYEIKYEQD-ENSYTIKSKETITTAEGKLPASVYVFOIRARTAGYGYFSRFE--- 558
QY 535 LEEASGKFEATV---SSBONPVYIIIAVAVAGTIIIVFVPGPII-----GRR- 581
DB 559 -----FETTPVFGASNDQSIPIGVSVTAVGIIIAVMI-GFLLSGSCCECGGRAS 609

QY 582 -----HCGYKADQEGDEE-LYFSLVTNHELSV 609
DB 610 SLCAVAHPSLIWRCGYSKAKQDPEEBKMHF---NGHKL 646

RESULT 9

receptor-tyrosine-protein-tyrosine kinase Cdk7, long splice form - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
A:Accession: 150615; 150616; 150614
R:Siever, D.A.; Verderame, M.F.
Gene 148, 219-226, 1994
A:Title: Identification of a complete Cdk7 receptor protein tyrosine kinase coding seque
A:Reference number: 150614; MUID:95047425; PMID:7958948
A:Accession: 150615
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1013 <SIR>
A:Cross-references: UNIPROT:P54755; EMBL:U03910; NID:9555617; PIDN:AAB60612.1; PID:95556
A:Accession: 150616
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-572, 'R', 596-1013 <S12>
A:Cross-references: EMBL:U03910; NID:9555617; PIDN:AAB60613.1; PID:9555619
A:Accession: 150614
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-279, 444-572, 'R', 596-1013 <S13>
A:Cross-references: EMBL:U03910; NID:9555617; PIDN:AAB60614.1; PID:9555620
C:Genetics:
A:Gene: Cdk7
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C:Keywords: alternative splicing; ATP; transmembrane protein
P:649-915/Domain: protein kinase homology <KIN>
P:657-665/Region: protein kinase ATP-binding motif
P:938-1004/Domain: SAM homology <SAM>

Query Match 55.6%; Score 1802; DB 2; Length 1013;
Best Local Similarity 53.3%; Pred. No. 3.9e-122;
Matches 347; Conservative 96; Mismatches 137; Indels 48; Gaps 10;

QY 8 PSW--IILCYIWLGFHTGEAQAKEVLLDSKAQTELEWISSPPSGMEISGLDENY 65
DB 15 PWTCLLCAALNSLASPG-----SEVNLDSRTVWGDIILAYPKNGEIEGVENDY 69
QY 66 TPRTYOVQVMEPNQNMRLTNWISKGNQRIFVELKFTLRDQNSLPGVLTCKETFTNL 125
DB 70 APHTYOVQVMEQONQNMRLTWSISMEGRPASSELKFTLRDQNSLPGVLTCKETFTNM 129
QY 126 YYYETDYDTRNIRENLVYKIDTIADESFTQDGLGRKKKLTVEAREIPLSKGYLA 185
DB 130 YYESDDEDRNIRENXYIKIDTIADESFTLEDGLGRVKKLTVEARDVPLTKGYLA 189
QY 186 FQDVGAICALVSVKYYKKCWTIVENLAVFPDPTVTSSEFSSLVEVRGCVS-SAEAEAN 244
DB 190 FQDVGAICALVSAVYKCKCPVYRNLAKEPDDITITGADSSQLLEVSQVCHNSTDEA-- 247
QY 245 SPRHCSAGEEMLVPIGCKICAGYQOKGDTCEPCGRFRFYSSQDLOCSRCPHTSFSR 304
DB 248 -PKHCSAGEEMLVPIGCKICAGYEEKNTQVCRGFPFASPHSPSCSKCPHSYTLTD 306
QY 305 EGSRCCEGCTYRABDPVPVACTRPPSPAPQNLIFINQTVLSLEWSPRPDNGRNDV 364
DB 307 EASTSCLEEHYFRESDEPTMACTRPPSPAPRNALISVNEISVLEWIPPADTGGRDVS 366
QY 365 YRIILCKRCSEWQECVPCGSNIGYMPQGTGLDNYVTVMILLAHANTFEVAVNGVSDL 424
DB 367 YRIILCKRCNSHGLCEACGSHVRYLPQOIGLKNISVMMADLATTNTFEIENVNGSDQ 426
QY 425 SRSORLFAVYSITGGAAPSOVSGVMEKERVLRVSQVLSMOEHPNVTITEYIKYKED 484

Db 427 NPGARQVSVNVTNNQAAPEPVSSVKKGKTKTKSISLSWQEPDRPNCIIIIYEIKYEKD 486
 QY 485 QRERTYSTLTKTSASINNLKPGTYVYFOIRAVTAAGYNGYSPRLDVATLEBASGMKPE 544
 Db 487 Q-ETSYTIISKETAIADGKPGSAVYVFOIRAVTAAGYNGYSPRLDVATLEBASGMKPE 537
 QY 545 ATAVSSQONVILIAVAVAGTITLVPMVPGFIIGRR-----H 582
 Db 538 VLAASSQSQSIPII-VVSVTVGVILIAVIGFLLSGSCDHDGCMASLRBAVAVPSLIWR 596
 QY 583 CGYSKADQEGDEE-LYFHSVLTNEHLSV 609
 Db 597 CGYSKADQEGDEE-MHPR---NGHITKL 620

RESULT 10

A38224
 protein-tyrosine kinase (EC 2.7.1.112) hek precursor - human
 C/Species: Homo sapiens (man)
 C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C/Accession: A38224; B38224
 R/Wicks, I.P.; Wilkerson, D.; Salvaris, E.; Boyd, A.W.
 Proc. Natl. Acad. Sci. U.S.A. 89, 1611-1615, 1992
 A/Title: Molecular cloning of HEK, the gene encoding a receptor tyrosine kinase expressed
 A/Reference number: A38224; MUID:92179233; PMID:1311845
 A/Accession: A38224
 A/Molecule type: mRNA
 A/Residues: 1-983 <WIC>
 A/Cross-references: UNIPROT:P29320; GB:M83941; NID:g183931; PIDN:AAA5863.1; PID:g183932
 A/Experimental source: pre-B-cell leukemia cell line LK63
 A/Note: sequence extracted from NCBI database (NCBI:86627)
 A/Accession: B38224
 A/Molecule type: protein
 A/Residues: 21-39/810-860 <M12>
 C/Keyfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
 C/Keywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferase;
 F:1/20/Domain: signal sequence #status predicted <SIG>
 F:21-983/Product: protein-tyrosine kinase hek #status experimental1 <MAT>
 F:542-565/Domain: transmembrane #status predicted <TM>
 F:619-685/Domain: protein kinase homology <KIN>
 F:627-635/Region: protein kinase ATP-binding motif
 F:232,337,391,404,493/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 55.5%; Score 1799; DB 2; Length 983;

Best Local Similarity 57.0%; Pred. No. 6.2e-122; Matches 332; Conservative 103; Mismatches 131; Indels 16; Gaps 6;

QY 28 QAAKEVLLDSKAQOTLEWISSPGMEISGLDENYETIRTYOVQWENPNNMLRT 87
 Db 25 QPSNEVLLDSKTIQGLGMIYSPSHGMEISGVDEHYTPRTYQVCNVMCHSQNNMLRT 84
 QY 88 NMISKGAQRIFVELKFTLRDQNSLPGLGTCKETPNLYYETDYDTRGRIRENTLYKID 147
 Db 85 NMPVPRNSAQKIYELKFTLRDQNSLPGLGTCKETPNLYYETDYDTRGRIRENTLYKID 144
 QY 148 TIAADESFTQGLDGERMKLNTVEIREGLSKGFIYAFODVACIALVSVKVYKKCW 207
 Db 145 TIAADESFTQGLDGERMKLNTVEIREGLSKGFIYAFODVACIALVSVKVYKKCP 204
 QY 208 IVNINLAVPRTYVSESSSLVEVRGTCVSAEBAENSPPMHGASABEEMLVPIGKCTCKA 267
 Db 205 TVKNLAFEPRTVP-MDSQSLVEVRGSCVNNSKS--EDPPMYCSTBEEMLVPIGKCSNA 261
 QY 268 GYOQKGTCEPCGRRPFYKSSSODLQCRPTHSFSDREGSRCEDEGGYVRAADSPYVA 327
 Db 262 GYERGGVCAACRGFKALDGNMKKCAKCFHSTQDGSNCRCEENYVRADKDPSPMA 321
 QY 328 CTRPPSPAPNULIFINOTVTSLEKSPADNGGRNDVYRILCKRCWEGECVPCGSNIG 387
 Db 322 CTRPPSPAPNULIFINOTVTSLEKSPADNGGRNDVYRILCKRCWEGECVPCGSNIV 381
 QY 388 YMGQOQGLENNYVWMDLHAHYTFEVAVNGVSDLSRQRLFAVSIITTGGAAPSOVS 447

Db 382 FLPRQGLNTVTVTDLHAHYTFEIDAIVNGVSELSBPPOFAVSTTNOAAPSVL 441
 QY 448 GWKKEVLAQRVOLSWQEPHPNGVITEYEIKYEKQRERTYSTLTKTSASINNLKP 507
 Db 442 TIKQDTRNSISLSWQEPHPNGIILDEVKYEKQRETSYTLIRAGTNTVISLKP 501
 QY 508 GTTYVFOIRAVTAAGYNGYSPRLDVATLEBASGMKPEATVASEQNPVILIAVAVAGT 567
 Db 502 DITYVFOIRAVTAAGYNGYSPRLDVATLEBASGMKPEATVASEQNPVILIAVAVAGT 554
 QY 568 ILVPMVPGFIIGRRHCGSKADQEGDEELYFHSVLTNEHLSV 609
 Db 555 LITVTVY-VLIG-RFCGYKSKGADKRIHF---GNGHITKL 590

RESULT 11

I51549
 receptor tyrosine kinase - African clawed frog
 C/Species: Xenopus laevis (African clawed frog)
 C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C/Accession: I51549
 R/Wimings, R.S.; Sargent, T.D.
 Mech. Dev. 46, 219-229, 1994
 A/Title: Pagliaccio, a member of the Eph family of receptor tyrosine kinase genes, has 1c
 A/Reference number: I51549; MUID:95001564; PMID:7918105
 A/Accession: I51549
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-985 <WIN>
 A/Cross-references: UNIPROT:Q91694; GB:I26099; NID:g416402; PIDN:AAA64464.1; PID:g416403
 A/Genetic:
 A/Gene: Pag
 C/Keyfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
 C/Keywords: ATP; transmembrane protein
 F:618-884/Domain: protein kinase homology <KIN>
 F:626-634/Region: protein kinase ATP-binding motif
 F:907-973/Domain: SHM homology <SHM>

Query Match 55.1%; Score 1788.5; DB 2; Length 985;

Best Local Similarity 57.6%; Pred. No. 3.6e-121; Matches 341; Conservative 93; Mismatches 145; Indels 13; Gaps 6;

QY 11 IILCYTMLQFATG-BAQAAKEVLLDSKAQOTLEWISSP-PSGMEISGLDENYTP 68
 Db 8 ILFCGIFGLCWAATGSRIPASEVTLIDRSVGBGLIASPLGMEISIMDEKNTPI 67
 QY 69 RTYOVQWENPNNMLRTNWKISKGAQRIFVELKFTLRDQNSLPGLGTCKETPNLYY 128
 Db 68 RTYOVQWENPNNMLRTNWKISKGAQRIFVELKFTLRDQNSLPGLGTCKETPNLYY 127
 QY 129 ETDYDTRGRIRENTLYKIDTIAADESFTQGLDGERMKLNTVEIREGLSKGFIYAFOD 188
 Db 128 ESNNDKERFIRETYQYKIDTIAADESFTQGLDGERMKLNTVEIREGLSKGFIYAFOD 187
 QY 189 VGACIALVSVKYYKKCWITVENLAFPTDVSSSSLVEVRGTCVSAEBAENSPPM 248
 Db 188 VGACIALVSVKYYKKCWITVENLAFPTDVSSSSLVEVRGTCVSAEBAENSPPM 245
 QY 249 HCSAEGEMLVPIGKCTCKAGYQKGTCEPCGRRPFYKSSSODLQCRPTHSFSDREGSS 308
 Db 246 YCGADEEMLVPIGKCTCKAGYQKGTCEPCGRRPFYKSSSODLQCRPTHSFSDREGSS 305
 QY 309 RCEDEGYVRAAPSDPEYVACTRPPSPAPNULIFINOTVTSLEKSPADNGGRNDVYRIL 368
 Db 306 SCICDRGTYRADTDPAISMCTRPPSPAPNULISVNETSVNLEWSPONGRPRDVSNTLV 365
 QY 369 CRRGSGEGECVPCGSNIGMPQOTLENNYVWMDLHAHYTFEVAVNGVSDLSRQ 428
 Db 366 CRRGSGDLTRCSPCGSGVHSPQONGLKTTKVISINDLAHTNTVFEVMAINGVSKQNP 425
 QY 429 RLFAAVSITTGGAAPSOVS GWKKEVLAQRVOLSWQEPHPNGVITEYEIKYEKQRE 488
 Db 426 DQAVSVTVITNOAAPSSTVIOQPKETTRHSVSLTMEPRANGVILIEYKYEKQNER 485

RESULT 14
I78844
receptor protein-tyrosine kinase - human
C/Species: Homo sapiens (man)
C/Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change (9-Jul-2004
C/Accession: I78844
R/Fox, G.M.; Holte, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, L.M.; Basu, R.; Welcher,
Oncogene 10, 897-905, 1995
A/Title: cDNA cloning and tissue distribution of five human Eph-like receptor protein-ty
A/Reference number: 158351; MUID:95206782; PMID:7898931
A/Accession: I78844
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-986 <RES>
A/Cross-references: UNIPROT:P54764; GB:IJ3645; NID:g551613; PIDN:AAA74246.1; PID:g551614
C/Genetics:
A/Genes: HEK8
C/Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
P,619-885/Domain: protein kinase homology <KIN>
F,908-974/Domain: SAM homology <SAM>

Query Match 53.5%; Score 1736.5; DB 2; Length 986;
Best Local Similarity 55.8%; Pred. No. 2,1e-117;
Matches 320; Conservative 107; Mismatches 133; Indels 3; Gaps 6;

QY 30 AKEVLLDSKAQOTLEWISSP-PSGWEISGLDENTYPIRTYQVCWMEPNQNNMLRTN 88
DB 28 ANEVTLLDSRSVOGELGIMASPLEGWEVSIIMDEKNTPIRTYQVCWME>SQNNMLRTD 87
QY 89 WISKNAQRIFVLLKFTLRDCLNSLPGLGCKETFNLYYETDYDGRNIRENLYKIDT 148
DB 88 WIREGQRVYIETKFTLRDCLNSLPGLGCKETFNLYYETDYDGRNIRENLYKIDT 147
QY 149 IADESFOTGLDERKMKLNTVEIREIGLSKGFYLAFOVGACIALVSVGVYKCKWTI 208
DB 148 IADESFOTGLDERKMKLNTVEIREIGLSKGFYLAFOVGACIALVSVGVYKCKWTI 207
QY 209 VENLAVPDPTVTGSEPSISLVEVGTCSAEEBAENSPRMCSAEGEMLVPIKCKICKAG 268
DB 208 VRLMAQFPDPTITGADTSILVEVGTCSAEEBAENSPRMCSAEGEMLVPIKCKICKAG 265
QY 269 YQCKGDTCEPCGRFRFYKSSQDQCSRCPTHSFSDRGSSRCCEGCVYVAPDPPVAC 328
DB 266 HEHRSRGCEQCKIGYVYALSTDAICACPHYSVWEGATSCTCDRPFPRADDAAMPC 325
QY 329 TRPSPAPQNLININQTTVLSLEWSPPADNGRNDVTYRIILCKRC-SWEOG3CVPCSGNIG 387
DB 326 TRPSPAPQNLININQTTVLSLEWSPPADNGRNDVTYRIILCKRC-SWEOG3CVPCSGNIG 385
QY 388 YMPQGTGLENDYVTVMDLAAHANTFEVAVNGVSDLSRSQRLPAVSIITGQAPSOVS 447
DB 386 YTPQOGLTKTKTISITDLAHNTYTFEIMAVNGVSKPNPDOSVSTVTVINDAASSIA 445
QY 448 GWKKEVLRQSVOLSMOEPHPNGVITEYIKYKEDQRETYSTLTKTSISASINMLKP 507
DB 446 LVQAKEVTRSVALLMEPRNGVILEVVKYKEDQRETYSTLTKTSISASINMLKP 505
QY 508 GTVYVFCIRAVTAAGYNSPRLDVATLEBASGMFEATVSSSEONVILIAVAVAGTI 567
DB 506 LTVYVHFVHARTAGVGDSEPLEYTT-----NTVPSRIIGGANSTVLL--VSVSGSV 557
QY 568 IL-VFMVFGFTIGRRHCGYSKADQEGDEELVYH 599
DB 568 VLVVILIAFVISRRSKYSKAKQEADEEKHLN 590

RESULT 15
S78059
protein-tyrosine kinase (EC 2.7.1.112) Eph precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C/Accession: S78059; S30505; I58366
R/Charnay, P.

submitted to the EMBL Data Library, March 1992
A/Reference number: S78059
A/Accession: S78059
A/Molecule type: mRNA
A/Residues: 1-986 <CHA>
A/Cross-references: UNIPROT:Q03137; EMBL:X65138; NID:g54083; PIDN:CAA6268.1; PID:g54084
R/Gillard, H.; Heberstreit, P.; Nito, M.A.; Frain, M.; Matzel, M.G.; Chastier, A.; Wilkinson,
Oncogene 7, 2499-2506, 1992
A/Title: An Eph-related receptor protein tyrosine kinase gene segmentally expressed in t
A/Reference number: S30496; MUID:93096484; PMID:1281307
A/Accession: S30505
A/Molecule type: mRNA
A/Residues: 1-31,55-986 <GTL>
A/Cross-references: EMBL:X65138
C/Genetics:
A/Genes: Sak
C/Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C/Keywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferase; t
F,1-15/Domain: signal sequence #status predicted <SIG>
F,16-986/Product: protein-tyrosine kinase Eph #status predicted <NAT>
F,548-569/Domain: transmembrane #status predicted <TM>
F,619-885/Domain: protein kinase homology <KIN>
F,627-635/Region: protein kinase ATP-binding motif
F,908-974/Domain: SAM homology <SAM>
F,235,340,408,423/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 53.0%; Score 1718; DB 2; Length 986;
Best Local Similarity 54.0%; Pred. No. 4,5e-116;
Matches 321; Conservative 113; Mismatches 146; Indels 14; Gaps 7;

QY 10 WITLCYIMLGFPHTC-EMQAKEVLLDSKAQOTLEWISSP-PSGWEISGLDENTYPT 67
DB 7 FILFSLFGICDAVTSRYVPAEVTLLDSRSVOGELGIMASPLEGWEVSIIMDEKNT 66
QY 68 IRTYQVCWMEPNQNNMLRTNMTSKGNAQRIFELKFTLRDCLNSLPGLGCKETFNLY 127
DB 67 IRTYQVCWMEPNQNNMLRTNMTSKGNAQRIFELKFTLRDCLNSLPGLGCKETFNLY 126
QY 128 YETDYDGRNIRENLYKIDTIADESFOTGLDERKMKLNTVEIREIGLSKGFYLAFO 187
DB 127 YESDNDKERFIRSGQKGTDTIADESFOTGLDERKMKLNTVEIREIGLSKGFYLAFO 186
QY 188 DVACIALVSVGVYKCKWTIYENLAVPDPTVTGSEPSISLVEVGTCSAEEBAENS 247
DB 187 DVACIALVSVGVYKCKWTIYENLAVPDPTVTGSEPSISLVEVGTCSAEEBAENS 244
QY 248 MHCSAEGEMLVPIKCKICKAGYQCKGDTCEPCGRFRFYKSSQDQCSRCPTHSFSD 307
DB 245 MHCSAEGEMLVPIKCKICKAGYQCKGDTCEPCGRFRFYKSSQDQCSRCPTHSFSD 304
QY 308 SRCECDGYRABSDPPVACTRPPSPAPQNLININQTTVLSLEWSPPADNGRNDVTY 367
DB 305 TSCTCDRGFPFRADDAAMPCRTTRPSPAPQNLININQTTVLSLEWSPPADNGRNDVTY 364
QY 368 LCKRC-SWEOG3CVPCSGNIGYMPQGTGLENDYVTVMDLAAHANTFEVAVNGVSD 426
DB 365 VCKKCGADGPSKCRPGSGVHYTPQOGLTKTKTISITDLAHNTYTFEIMAVNGVSK 424
QY 427 SORLPAVSIITGQAPSOVSQVGMKERVLRQSVOLSMOEPHPNGVITEYIKYKEDQ 486
DB 425 SPQSVSVITVTTQAPSSIALVQAKETRYVALALMEPRNGVILEVVKYKEDQ 484
QY 487 ERTYVSTLTKTSISASINMLKPGTVVFOIRAVTAAGYNSPRLDVATLEBASGMFEAT 546
DB 485 ERGYSRIVRTAARTDICKANPLTSYVHFVHARTAGVGDSEPLEYTT-----NTVPSR 538
QY 547 AVSSEONPVILIAVAVAGTII-VFMVFGFTIGRRHCGYSKADQEGDEELVYH 599
DB 539 IIGDGANSTVLL--VSVSGSVLVVILIAFVISRRSKYSKAKQEADEEKHLN 590

Search completed: August 23, 2005, 08:33:10
Job time : 18.2864 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 23, 2005, 08:26:40 ; Search time 70.5744 Seconds

(without alignments)
4426.083 Million cell updates/sec

Title: US-10-073-064-3

Perfect score: 3243
Sequence: 1 MVVQTRPPSWILLCYIWLGL.....EGDELYFHSIVTNEHLSVL 610

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|--------------|--------------------|
| 1 | 3239 | 99.9 | 610 | 2 Q8CC52 | Q8CC52 mus musculu |
| 2 | 3191 | 98.4 | 998 | 1 EPB7 MOUSE | Q61772 mus musculu |
| 3 | 3188 | 98.3 | 994 | 2 Q8R3B1 | Q8R3B1 mus musculu |
| 4 | 3187 | 98.3 | 998 | 2 Q8BSU8 | Q8BSU8 mus musculu |
| 5 | 3175 | 97.9 | 998 | 2 EPB7 RAT | P54759 ratu norv |
| 6 | 3139 | 96.8 | 998 | 1 EPB7 HUMAN | Q15375 mus musculu |
| 7 | 3126 | 96.4 | 993 | 2 Q8C7N2 | Q8C7N2 mus musculu |
| 8 | 3031.5 | 93.5 | 993 | 1 EPB7 CHICK | Q42422 gallu gall |
| 9 | 1862.5 | 57.4 | 681 | 2 Q8C276 | Q8C276 mus musculu |
| 10 | 1821 | 56.2 | 1005 | 1 EPB5 RAT | P54757 ratu norv |
| 11 | 1819 | 56.1 | 1037 | 1 EPB5 HUMAN | P54756 homo saplen |
| 12 | 1802 | 55.6 | 984 | 1 Q8BRB1 | Q8BRB1 mus musculu |
| 13 | 1802 | 55.6 | 1013 | 1 EPB5 CHICK | P54755 gallu gall |
| 14 | 1799 | 55.5 | 983 | 1 EPB3 HUMAN | P29320 homo saplen |
| 15 | 1799 | 55.5 | 983 | 2 Q6P4R6 | Q6P4R6 homo saplen |
| 16 | 1798 | 55.4 | 984 | 2 Q8C3U1 | Q8C3U1 mus musculu |
| 17 | 1793.5 | 55.3 | 986 | 1 EPB4 XENLA | Q1845 xenopus lae |
| 18 | 1790 | 55.2 | 969 | 2 Q7Z3R2 | Q7Z3R2 homo saplen |
| 19 | 1789.5 | 55.2 | 984 | 1 EPB3 RAT | Q06680 ratu norv |
| 20 | 1788.5 | 55.1 | 985 | 1 EPB4 XENLA | Q91694 xenopus lae |
| 21 | 1787.5 | 55.1 | 986 | 2 Q7ZVM7 | Q7ZVM7 xenopus lae |
| 22 | 1786.5 | 55.1 | 983 | 1 EPB3 CHICK | P29318 gallu gall |
| 23 | 1786.5 | 55.1 | 983 | 1 EPB3 MOUSE | P29319 mus musculu |
| 24 | 1747.5 | 53.9 | 986 | 1 EPB4 CHICK | Q07496 gallu gall |
| 25 | 1739 | 53.6 | 538 | 2 Q8C9K6 | Q8C9K6 mus musculu |
| 26 | 1736.5 | 53.5 | 986 | 1 EPB4 HUMAN | P54764 homo saplen |
| 27 | 1723 | 53.1 | 986 | 2 Q8OVZ2 | Q8OVZ2 mus musculu |
| 28 | 1718 | 53.0 | 986 | 1 EPB4 MOUSE | Q03137 mus musculu |
| 29 | 1701.5 | 52.5 | 1005 | 1 EPB8 HUMAN | P29322 homo saplen |
| 30 | 1695 | 52.3 | 1004 | 1 EPB6 MOUSE | Q09127 mus musculu |
| 31 | 1662 | 51.2 | 948 | 1 EPB6 RAT | P54758 ratu norv |

| | | | | | |
|----|--------|------|------|--------------|--------------------|
| 32 | 1652 | 50.9 | 976 | 2 Q902N9 | Q902N9 brachydanio |
| 33 | 1651 | 50.9 | 1035 | 1 EPB6 MOUSE | Q62413 mus musculu |
| 34 | 1631 | 50.3 | 981 | 1 EPB3 BRABE | Q3146 brachydanio |
| 35 | 1625 | 50.1 | 927 | 2 Q99KX8 | Q99KX8 mus musculu |
| 36 | 1590 | 49.0 | 880 | 2 Q73879 | Q73879 brachydanio |
| 37 | 1496 | 46.1 | 1004 | 1 EPB2 CHICK | P28693 gallu gall |
| 38 | 1477 | 45.5 | 994 | 1 EPB2 MOUSE | P54763 mus musculu |
| 39 | 1475 | 45.5 | 1055 | 1 EPB2 HUMAN | P29323 homo saplen |
| 40 | 1474 | 45.5 | 1021 | 2 Q6GTQ7 | Q6GTQ7 mus musculu |
| 41 | 1470 | 45.3 | 987 | 1 EPB2 COTUA | Q90344 coturnix co |
| 42 | 1465.5 | 45.2 | 1029 | 2 Q6P5F1 | Q6P5F1 mus musculu |
| 43 | 1458 | 45.0 | 279 | 2 Q8N368 | Q8N368 homo saplen |
| 44 | 1449 | 44.7 | 984 | 1 EPB1 RAT | P09759 ratu norv |
| 45 | 1448.5 | 44.7 | 984 | 1 EPB1 HUMAN | P54762 homo saplen |

ALIGNMENTS

| RESULT 1 | ID | Q8CC52 | PRELIMINARY; | PRT; | 610 AA. |
|----------|---|--------|--------------|------|---------|
| AC | Q8CC52 | | | | |
| DT | 01-MAR-2003 (TREMBLrel. 23, Created) | | | | |
| DT | 01-MAR-2003 (TREMBLrel. 23, Last sequence update) | | | | |
| DT | 01-MAR-2004 (TREMBLrel. 26, Last annotation update) | | | | |
| DE | Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched library, clone:330112M11 product:Bph receptor A7, full insert | | | | |
| DE | sequence. | | | | |
| GN | Name=Epha7; | | | | |
| OS | Mus musculus (Mouse). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | | |
| OX | NCBI TaxID=10090; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN=C57BL/6J; TISSUE=Diencephalon; | | | | |
| RE | MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; | | | | |
| RA | Carninci P., Hayashizaki Y.; | | | | |
| RT | "High-efficiency full-length cDNA cloning."; | | | | |
| RL | Nature 409:685-690(2001). | | | | |
| RN | [3] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN=C57BL/6J; TISSUE=Diencephalon; | | | | |
| RA | The FANTOM Consortium, | | | | |
| RT | "the RIKEN Genome Exploration Research Group Phase I & II Team; | | | | |
| RL | "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; | | | | |
| RL | Nature 420:563-573(2002). | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN=C57BL/6J; TISSUE=Diencephalon; | | | | |
| RE | MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; | | | | |
| RA | Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., | | | | |
| RT | Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.; | | | | |
| RT | "Normalization and subtraction of cap-trapper-selected cDNAs to | | | | |
| RT | prepare full-length cDNA libraries for rapid discovery of new genes."; | | | | |
| RL | Genome Res. 10:1617-1630(2000). | | | | |
| RN | [5] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | STRAIN=C57BL/6J; TISSUE=Diencephalon; | | | | |
| RE | MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; | | | | |
| RA | Shibata K., Itoh M., Aizawa K., Nagoka S., Sasaki N., Carninci P., | | | | |
| RA | Kono H., Akiyama J., Nishi K., Kitsumi T., Tashiro H., Itoh M., | | | | |
| RA | Sun N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A., | | | | |
| RA | Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishiwagi K., | | | | |

| | | | | |
|----|----------|-----|-----|---|
| FT | TRANSMEM | 557 | 577 | Potential. |
| FT | DOMAIN | 578 | 998 | Cytoplasmic (Potential). |
| FT | DOMAIN | 192 | 328 | Cys-rich. |
| FT | DOMAIN | 331 | 433 | Fibronectin type-III 1. |
| FT | DOMAIN | 443 | 535 | Fibronectin type-III 2. |
| FT | DOMAIN | 633 | 894 | Protein kinase. |
| FT | DOMAIN | 923 | 987 | SAM. |
| FT | SITE | 996 | 998 | PDZ-binding motif (Potential). |
| FT | NP BIND | 639 | 647 | ATP (By similarity). |
| FT | BINDING | 665 | 665 | ATP (By similarity). |
| FT | ACT_SITE | 758 | 758 | By similarity. |
| FT | MOD_RES | 608 | 608 | Phosphotyrosine (by autocatalysis) (Potential). |
| FT | MOD_RES | 614 | 614 | Phosphotyrosine (by autocatalysis) (Potential). |
| FT | MOD_RES | 791 | 791 | Phosphotyrosine (by autocatalysis) (Potential). |
| FT | MOD_RES | 940 | 940 | Phosphotyrosine (by autocatalysis) (Potential). |
| FT | CARBOHYD | 64 | 64 | N-linked (GlcNAc. . .) (Potential). |
| FT | CARBOHYD | 343 | 343 | N-linked (GlcNAc. . .) (Potential). |
| FT | CARBOHYD | 410 | 410 | N-linked (GlcNAc. . .) (Potential). |
| FT | VARSPLIC | 540 | 544 | Missing (in isoform 2). |
| FT | VARSPLIC | 601 | 604 | /FtId=VSP_003006. |
| FT | VARSPLIC | 600 | 610 | Missing (in isoform 3). |
| FT | VARSPLIC | 600 | 610 | /FtId=VSP_003007. |
| FT | VARSPLIC | 611 | 998 | EKFGGTGYTID -> SLVTNHEHLSVL (in isoform 4). |
| FT | VARSPLIC | 600 | 626 | Missing (in isoform 4). |
| FT | VARSPLIC | 627 | 998 | /FtId=VSP_003009. |
| FT | VARSPLIC | 627 | 998 | EKFGGTGYTIDPETEDPNRAVHOFAK -> SLYRERGDM |
| FT | VARSPLIC | 627 | 998 | EKTQHNKKMMWASCSRL (in isoform 5). |
| FT | VARSPLIC | 627 | 998 | /FtId=VSP_003010. |
| FT | VARSPLIC | 627 | 998 | Missing (in isoform 5). |
| FT | VARSPLIC | 627 | 998 | /FtId=VSP_003011. |
| FT | VARSPLIC | 627 | 998 | Y -> H (in Ref. 2). |
| FT | VARSPLIC | 627 | 998 | /FtId=VSP_003012. |
| FT | VARSPLIC | 627 | 998 | /FtId=VSP_003013. |
| FT | VARSPLIC | 627 | 998 | /FtId=VSP_003014. |
| FT | VARSPLIC | 627 | 998 | /FtId=VSP_003015. |
| FT | VARSPLIC | 627 | 998 | /FtId=VSP_003016. |
| FT | VARSPLIC | 627 | 998 | /FtId=VSP_003017. |
| FT | VARSPLIC | 627 | 998 | /FtId=VSP_003018. |
| FT | VARSPLIC | 627 | 998 | /FtId=VSP_003019. |
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| FT | VARSPLIC | 627 | 998 | /FtId=VSP_003043. |
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| FT | VARSPLIC | 627 | 998 | /FtId=VSP_003047. |
| FT | VARSPLIC | 627 | 998 | /FtId=VSP_003048. |
| FT | VARSPLIC | 627 | 998 | /FtId=VSP_003049. |
| FT | VARSPLIC | 627 | 998 | /FtId=VSP_003050. |
| FT | VARSPLIC | 627 | 998 | /FtId=VSP_003051. |
| FT | VARSPLIC | 627 | 998 | /FtId=VSP_003052. |
| FT | VARSPLIC | 627 | 998 | /FtId=VSP_003053. |
| FT | VARSPLIC | 627 | 998 | /FtId=VSP_003054. |
| FT | VARSPLIC | 627 | 998 | /FtId=VSP_003055. |
| FT | VARSPLIC | 627 | 998 | /FtId=VSP_003056. |
| FT | VARSPLIC | 627 | 998 | /FtId=VSP_003057. |
| FT | VARSPLIC | 627 | 998 | /FtId=VSP_003058. |
| FT | VARSPLIC | 627 | 998 | /FtId=VSP_003059. |
| FT | VARSPLIC | 627 | 998 | /FtId=VSP_003060. |
| FT | VARSPLIC | 627 | 998 | |

Db 421 VSDLSRQRLFAVSTTGOAPBSQVSGWVKERVLORSVOLSQWDEPHNGVITEYIKY 480
 QY 481 YEKDQERTYSTLTKTSTASINNLKPGTYVYFOIRAVTAAGYNSPRLVATLEBASG 540
 Db 481 YEKDQERTYSTLTKTSTASINNLKPGTYVYFOIRAVTAAGYNSPRLVATLEBASG 540
 QY 541 KMEFATVSSSEONPVIIIAVAVAGTIIIVFWFGFIIGRRHGYSKADQIGDELYFH 599
 Db 541 KMEFATVSSSEONPVIIIAVAVAGTIIIVFWFGFIIGRRHGYSKADQIGDELYFH 599
 RESULT 3
 Q8R381 PRELIMINARY; PRT; 994 AA.
 AC Q8R381;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Epha7 protein.
 GN Name=Epha7;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C26CH II; TISSUE=Mammary tumor;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derse J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Gancini P., Pringle C.,
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulady S.J.,
 RA Beek S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richardson S., Wotley K.C., Hale S., Garcia A.M., Gay L.U., Gibbs R.A.,
 RA Villalón D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Halton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Touchman J.W., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywnicki M.I., Skalska U., Smalins D.E., Schnerch A., Schain J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C26CH II; TISSUE=Mammary tumor;
 RA Strausberg R.;
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin
 receptor subfamily.
 DR EMBL: BC026153; AAH26153.1; -.
 DR HSSP: P54763.1JPA.
 DR MGD: MGI.95276; Epha7.
 DR GO: GO:0005615; C:intracellular space; TAS.
 DR GO: GO:0016021; C:integral to membrane; TAS.
 DR InterPro: IPR006209; EGF_1like.
 DR InterPro: IPR01090; Ephrin receptor.
 DR InterPro: IPR003962; FhII subd.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR008957; FN_III-1like.
 DR InterPro: IPR008979; Gal_bind_1like.
 DR InterPro: IPR009030; Grow_fac_recept.
 DR InterPro: IPR011009; kinase_1like.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR001660; SAM.

DR InterPro: IPR001245; Tyr_kinase.
 DR InterPro: IPR008266; Tyr_kinase_AS.
 DR InterPro: IPR001426; YKase_receptor_v.
 DR Pfam: PF01404; Ephrin_1bd; 1.
 DR Pfam: PF00041; fn3_1.
 DR Pfam: PF00536; SAM_1.1.
 DR PRINTS: PR00014; ENTPEIIT.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD001495; Ephrin_receptor; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00615; EPH_1bd; 1.
 DR SMART: SM00060; FN3_2.
 DR SMART: SM00454; SAM; 1.
 DR SMART: SM00219; TYKc; 1.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS50853; FN3_2.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE: PS50105; SAM_DOMAIN; 1.
 DR ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;
 KW Transferase; Transmembrane; Tyrosine-protein kinase
 SQ SEQUENCE 994 AA; 111386 MW; A28F98BD964F2EB8 CRC64;

Query Match 98.3%; Score 3188; DB 2; Length 994;
 Best Local Similarity 99.3%; Pred. No. 1.5e-230;
 Matches 599; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MVQTPSPKIIICITWLGFAHTGAQAKEYLLDLSAQOQTELEWISSPSPGWEISG 60
 Db 1 MVQTFPPSIIICITWLGFAHTGAQAKEYLLDLSAQOQTELEWISSPSPGWEISG 60
 QY 1DENYPIRTIYQCVQWEPNUNNMLRTNMIISKNAORIFVELKFTLRDNCSLPGVIGTCK 120
 Db 1DENYPIRTIYQCVQWEPNUNNMLRTNMIISKNAORIFVELKFTLRDNCSLPGVIGTCK 120
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 Db 121 EFNLLYYETDVTGDNIRENLVYKIDTIADESFTQDGLGERKMLNTEVREIGPLSKK 180
 QY 181 GFPLAODVQACIALVSVYVYKKWTIVENLAFPDYTTGSSFLVEVRCVSSARE 240
 Db 181 GFPLAODVQACIALVSVYVYKKWTIVENLAFPDYTTGSSFLVEVRCVSSARE 240
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 Db 241 EAENSFRMCSABGEMLVPIGKICICAGYQOKGDTCEPCGRPYKSSSODLQCSRCPTHS 300
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 Db 301 FSDREGSSRCECDGYRAAPSDPYVACTRPSPAPONTLEPQOTTVLSLEWSPADNGR 360
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 QY 421 VSDLSRQRLFAVSTTGOAPBSQVSGWVKERVLORSVOLSQWDEPHNGVITEYIKY 480
 Db 421 VSDLSRQRLFAVSTTGOAPBSQVSGWVKERVLORSVOLSQWDEPHNGVITEYIKY 480
 QY 481 YEKDQERTYSTLTKTSTASINNLKPGTYVYFOIRAVTAAGYNSPRLVATLEBASG 540
 Db 481 YEKDQERTYSTLTKTSTASINNLKPGTYVYFOIRAVTAAGYNSPRLVATLEBASG 540
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 Db 541 KMEFATVSSSEONPVIIIAVAVAGTIIIVFWFGFIIGRRHGYSKADQIGDELYFH 600
 QY 601 LVT 603
 Db 601 TKT 603

RESULT 4
Q8BSUS PRELIMINARY; PRT: 998 AA.
AC Q8BSUS;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male pituitary gland cDNA, RIKEN full-length
DE enriched library, clone:5330417H08 product:Eph receptor A7, full
DE insert sequence.
GN Name=Sphe7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=pituitary gland;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=pituitary gland;
RX MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT Nature 420:563-573(2002)."
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=pituitary gland;
RX MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT Prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=pituitary gland;
RX MEDLINE=20505913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitounai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kaishiwagi K.,
RA Fujisake S., Inoue K., Togawa Y., Izawa M., Ohara E., Matshiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai U.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=pituitary gland;
RA Aachti J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata N., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin
CC receptor subfamily.
DR EMBL: AK030480; BAC26982.1; -.
DR HSSP: P54763; ITPA.
DR MGJ: MGJ:95276; Epha7.
DR GO: GO:0005615; C:extracellular space; TAS.
DR GO: GO:0016021; C:integral to membrane; TAS.
DR InterPro: IPR006209; EGF_1ike.
DR InterPro: IPR001090; Ephrin_receptor.
DR InterPro: IPR003962; FNIII_subd.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III_1like.
DR InterPro: IPR008979; Gal_bind_1like.
DR InterPro: IPR009030; Grow_fac_recept.
DR InterPro: IPR011009; kinase_1like.
DR InterPro: IPR007019; Prot_kinase.
DR InterPro: IPR001245; SAM.
DR InterPro: IPR008266; Tyr_kinase_AS.
DR InterPro: IPR001426; Ykase_receptorV.
DR Pfam: PF01404; Ephrin_1bdt.1.
DR Pfam: PF00041; Fn3_1.
DR Pfam: PF00536; SAM_1; 1.
DR PRINTS: PR00104; FNTYPEIII.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD001495; Ephrin_receptor; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00615; Eph_1bdt.1.
DR SMART: SM00060; FN3_2.
DR SMART: SM00454; SAM; 1.
DR SMART: SM00219; TYKc; 1.
DR PROSITE: PS001166; EGF_2; 1.
DR PROSITE: PSS0853; FN3_2; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE: PSS0105; SAM_DOMAIN; 1.
KW ATP-binding; Glycoprotein; Kinase; Phosphorylation; Receptor;
KW Transferrase; Transmembrane; Tyrosine-protein kinase.
SQ SEQUENCE 998 AA; 11859 MW; FCA1E83490E746E1 CRC64;
Query Match 98.3%; Score 3187; DB 2; Length 998;
Best Local Similarity 99.8%; Pred. No. 1.8e-230;
Matches 598; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVVQTPSPVSIICVYLWLGFAHTGEQAQAEVLLDLSKAQOTELEWISSPPSGMERISG 60
Db 1 MVVQTRPSPVSIICVYLWLGFAHTGEQAQAEVLLDLSKAQOTELEWISSPPSGMERISG 60
QY 61 LDENVYPIRTYQVCQWEPNQNWLRTNWSKNAQRIPELKFETLDDCNLSPLVIGCTCK 120
Db 61 LDENVYPIRTYQVCQWEPNQNWLRTNWSKNAQRIPELKFETLDDCNLSPLVIGCTCK 120
QY 121 EFTNLVYFETDPTGGRIRRENLVYKIDITLADSSFTQGDIGERKMKNTVREIGPSLCK 180
Db 121 EFTNLVYFETDPTGGRIRRENLVYKIDITLADSSFTQGDIGERKMKNTVREIGPSLCK 180
QY 181 GFYLAPODVACIALSVKYYKKCWITVENLAVPDTVTGSEFSSLVEVRCVSSAAE 240
Db 181 GFYLAPODVACIALSVKYYKKCWITVENLAVPDTVTGSEFSSLVEVRCVSSAAE 240
QY 241 EAENSPRMHCSAAGEWLVPIGKICIKAGYQOKGDTCPCGRPRFYKSSSDQLQCSRCPHTS 300
Db 241 EAENSPRMHCSAAGEWLVPIGKICIKAGYQOKGDTCPCGRPRFYKSSSDQLQCSRCPHTS 300

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QY 301 FSDREGSSRCEDGYRRASDPPEYVACTPPSAPQNLININQTVLSLEWSPADNGR 360
Db 301 FSDREGSSRCEDGYRRASDPPEYVACTPPSAPQNLININQTVLSLEWSPADNGR 360
QY 361 NDVTYRLCRGCGMEQECPCPGSNIGYMPQOGLBNYTWMDLAAHYTEVEAVNG 420
Db 361 NDVTYRLCRGCGMEQECPCPGSNIGYMPQOGLBNYTWMDLAAHYTEVEAVNG 420
QY 421 VSDLSRSQRLFAVSIITGGAAPSOVGWAKERVOLSNQEPHPNGVITEYIKY 480
Db 421 VSDLSRSQRLFAVSIITGGAAPSOVGWAKERVOLSNQEPHPNGVITEYIKY 480
QY 481 YEKDQRRRTYSTKTSTSSASINNLKPGTVYFQIRAVTAAGYGNVSPRLDVAITLEBASG 540
Db 481 YEKDQRRRTYSTKTSTSSASINNLKPGTVYFQIRAVTAAGYGNVSPRLDVAITLEBASG 540
QY 541 KMFEATVASEQNPVITIAVAVAGTIIIVMWPGFIIGRRHCGYSKADGEGBELYFH 599
Db 541 KMFEATVASEQNPVITIAVAVAGTIIIVMWPGFIIGRRHCGYSKADGEGBELYFH 599

RESULT 5
EPAT_RAT STANDARD; PRT; 998 AA.
ID P54759;
AC P54759;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ephrin type-A receptor 7 precursor (EC 2.7.1.112) (Tyrosine-protein
DE kinase receptor EHK-3) (Eph homolog kinase-3).
GN Name=EphA7; Synonyms=Ehk-3, Ehk3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RX MEDLINE=95249272; Pubmed=7731712;
RA Valenzuela D.M., Rojas E., Griffiths J.A., Compton D.L., Gisser M.,
RA Ip N.Y., Goldfarb M., Yancopoulos G.D.;
RT "Identification of full-length and truncated forms of Ehk-3, a novel
RT member of the Eph receptor tyrosine kinase family."
RL Oncogene 10:1573-1580(1995).
CC -1- FUNCTION: Receptor for members of the ephrin-A family. Binds to
CC ephrin-A1, -A2, -A3, -A4 and -A5.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBUNIT: Interacts with PRKCAP and GRIP1 (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=P54759-1; Sequence=Displayed;
CC Note=More widely expressed in the embryo;
CC Name=Short;
CC IsoId=P54759-2; Sequence=VSP_003012;
CC -1- Note=Lacks the kinase domain;
CC -1- TISSUE SPECIFICITY: Restricted to the nervous system.
CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin
CC receptor subfamily.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL, U21954; AAA86830.1; -.

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DR EMBL, U21955; AAA86831.1; -.
DR HSSP; P54763; 1JPA.
DR RGD; 70957; EphA7.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001090; Ephrin receptor.
DR InterPro; IPR003964; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003962; FNIII_subd.
DR InterPro; IPR008979; Gal_bind like.
DR InterPro; IPR009030; Grow_fac_recept.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001660; SAM.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR InterPro; IPR001426; YKase_receptorV.
DR Pfam; PF01404; Ephrin_1bd; 1.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00659; Pkinase; 1.
DR Pfam; PF00536; SAM; 1.
DR PRINTS; PR00014; ENTPEIIT.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD001495; Ephrin_receptor; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00615; Eph_1bd; 1.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00454; SAM; 1.
DR SMART; SM00219; TYRKc; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PSS0853; FN3_2; UNKNOWN_1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PSS0105; SAM_DOMAIN_1.
DR Alternative splicing; ATP-binding; Glycoprotein; Phosphorylation;
DR Receptor; Repeat; Signal; Transferase; Transmembrane;
KW Tyrosine-protein kinase.
FT SIGNAL 1 24
FT CHAIN 25 998
FT DOMAIN 25 556
FT TRANSMEM 557 577
FT TRANSMEM 578 998
FT DOMAIN 192 328
FT DOMAIN 331 433
FT DOMAIN 443 535
FT DOMAIN 633 894
FT DOMAIN 923 987
FT SITE 996 998
FT NP_BIND 639 647
FT BINDING 665 665
FT ACT_SITE 758 758
FT MOD_RES 608 608
FT MOD_RES 614 614
FT MOD_RES 614 614
FT MOD_RES 791 791
FT MOD_RES 940 940
FT CARBOHYD 343 343
FT CARBOHYD 410 410
FT VARSPIC 600 610
FT SQ SEQUENCE 998 AA; 111953 MW; A7A82A698924876C CRC64;

Query Match 97.9%; Score 3175; DB 1; Length 998;
Best Local Similarity 99.2%; Pred. No. 1,4e-229;
Matches 594; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 MVQTRPPSWITLCYIWLIGFAHTGEAQAKEYLLDLSKAQOTLEWISSPPSGWEISG 60

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Db      1  MVTQTRYSWIIILCYIMLGFHAGTGEADPAAEVLLLSKAOQTELEWISSPPSGWEETSG 60
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Db      61  LDEVTPIRTYQVCQVMEPNQNMWLRTWISKGNARFVELKPLRDQNSLPGLTGCK 120
Qy      121  ETEFLYYEYEDYDTRGRIRENLVYKIDITIADESFTQDGERKMKLNTREIREIGPLSK 180
Db      121  ETEFLYYEYEDYDTRGRIRENLVYKIDITIADESFTQDGERKMKLNTREIREIGPLSK 180
Qy      181  GFYIAPFDVGCIALVSVKYVKKCWITVENLAFPPDTVTSSPSLSLVEFGTGVSSAE 240
Db      181  GFYIAPFDVGCIALVSVKYVKKCWITVENLAFPPDTVTSSPSLSLVEFGTGVSSAE 240
Qy      241  EAENSPPHNCASGESEMLVPIGKICIKAGYQKQDTCPCRCGRFKSSGODIQSCRPHS 300
Db      241  EAENSPPHNCASGESEMLVPIGKICIKAGYQKQDTCPCRCGRFKSSGODIQSCRPHS 300
Qy      301  FSDREGSSRCCEDEGYRAPSDPYVACTRPPSAPOULIFNINOTVLSLEWSPPADNGR 360
Db      301  FSDREGSSRCCEDEGYRAPSDPYVACTRPPSAPOULIFNINOTVLSLEWSPPADNGR 360
Qy      361  NDVTYRILCKRCSEWQECVPCGSGNIGMPQOTGLENDYTVMDLLAHANTTFEVAVG 420
Db      361  NDVTYRILCKRCSEWQECVPCGSGNIGMPQOTGLENDYTVMDLLAHANTTFEVAVG 420
Qy      421  VSDLSRSORLFAAVSITTTGAAPSOVSVMWERLQORSVQSLQKQEPHEPNVITEYEKY 480
Db      421  VSDLSRSORLFAAVSITTTGAAPSOVSVMWERLQORSVQSLQKQEPHEPNVITEYEKY 480
Qy      481  YEKQQRERTYSTLTSTKSTASINNLKPGTVYFQIRAVTAAGYNGSPRLDVATLEASG 540
Db      481  YEKQQRERTYSTLTSTKSTASINNLKPGTVYFQIRAVTAAGYNGSPRLDVATLEASG 540
Qy      541  KMFPAIVSSQONPVIIIAVAVAGTIIIVMFQFIIGRRHCYSRADQGEDELYFH 599
Db      541  KMFPAIVSSQONPVIIIAVAVAGTIIIVMFQFIIGRRHCYSRADQGEDELYFH 599

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CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- TISSUE SPECIFICITY: widely expressed.
CC      -1- SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin
CC      receptor subfamily.
CC      -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC      -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.ldb-sib.ch/announce/
CC      or send an email to license@ldb-sib.ch).
CC      -----
CC      EMBL: L36642; AAA74243.1; -.
CC      EMBL: AL121966; CAC19520.1; -.
CC      PIR: I58351; I58351.
CC      HSSP: P54763; IUPA.
CC      Genew: HGNC:3390; EPHA7.
CC      MIM: 602190; -.
CC      GO: 0004714; F:transmembrane receptor protein tyrosine kin. . .; TMS.
CC      InterPro: IPR006209; EGF-like.
CC      InterPro: IPR001090; Ephrin_receptor.
CC      InterPro: IPR003961; FN III.
CC      InterPro: IPR008957; FN III-like.
CC      InterPro: IPR003962; FNIII subd.
CC      InterPro: IPR008979; Gal_bind-like.
CC      InterPro: IPR009030; Grow_fac_recept.
CC      InterPro: IPR011009; Kinase-like.
CC      InterPro: IPR007119; Prot_kinase.
CC      InterPro: IPR001660; SAM.
CC      InterPro: IPR001245; Tyr_kinase.
CC      InterPro: IPR008265; Tyr_kinase_AS.
CC      InterPro: IPR001426; Ykase_receptor.
CC      Pfam: PF01404; Ephrin_1bd; 1.
CC      Pfam: PF00041; fn3; 2.
CC      Pfam: PF00069; Pkinase; 1.
CC      Pfam: PF00536; SAM; 1.
CC      PRINTS: PR00014; ENTPEP11.
CC      PRINTS: PR00109; TYRKINASE.
CC      ProDom: PD001495; Ephrin_receptor; 1.
CC      ProDom: PD000001; Prot_kinase; 1.
CC      SMART: SM00645; EPH_1bd; 1.
CC      SMART: SM00060; FN3; 2.
CC      SMART: SM00454; SAM; 1.
CC      SMART: SM00219; TYRK; 1.
CC      PROSITE: PS01186; EGF_2; UNKNOWN_1.
CC      PROSITE: PS01853; FN3; 2.
CC      PROSITE: PS00107; PROTEIN KINASE ATP; 1.
CC      PROSITE: PS00107; PROTEIN KINASE_DOM; 1.
CC      PROSITE: PS00109; PROTEIN KINASE_TYR; 1.
CC      PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
CC      PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
CC      PROSITE: PS5105; SAM DOMAIN; 1.
CC      ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat; Signal;
CC      Transmembrane; Tyrosine-protein kinase.
CC      SIGNAL: 1 24
CC      CHAIN: 1 25 998
CC      DOMAIN: 25 556
CC      TRANSMEM: 557 577
CC      DOMAIN: 578 998
CC      DOMAIN: 192 328
CC      DOMAIN: 331 433
CC      DOMAIN: 443 535
CC      DOMAIN: 633 894
CC      DOMAIN: 923 987
CC      SITE: 996 998
CC      NP_BIND: 639 647
CC      BINDING: 665 665
CC      ACT_SITE: 758 758
CC      MOD_RES: 608 608

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RESULT 6
EPAT_HUMAN
ID      EPHA7_HUMAN          STANDARD;          PRT;          998 AA.
AC      Q15375; O9H124;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Ephrin type-A receptor 7 precursor (EC 2.7.1.112) (Tyrosine-protein
DE      kinase receptor EHK-3) (Eph homology kinase-3) (Receptor protein-
DE      tyrosine kinase HEK11).
GN      Name=EPHA7; Synonyms=EHK3, HEK11;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxId=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Fetal brain;
RX      MEDLINE=95206782; PubMed=7898931;
RA      Fox G.M., Holst P.L., Chute H.T., Lindberg R.A., Janssen A.M.,
RA      Baeu R., Welcher A.A.;
RT      "cDNA cloning and tissue distribution of five human EPH-like receptor
RT      protein-tyrosine kinases";
RL      Oncogene 10:897-905(1995).
RN      [2]
RP      SEQUENCE OF 1-277 FROM N.A.
RA      Bates K.;
RL      Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: Receptor for members of the ephrin-A family. Binds to
CC      ephrin-A1, -A2, -A3, -A4 and -A5.
CC      -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC      tyrosine phosphate.
CC      -1- SUBUNIT: Interacts with PRKCBP and GRIP1 (By similarity).

```



```

FT MOD_RES 614 614 Phosphotyrosine (by autocalysis)
FT (Potential)
FT MOD_RES 791 791 Phosphotyrosine (by autocalysis)
FT (Potential)
FT MOD_RES 940 940 Phosphotyrosine (by autocalysis)
FT (Potential)
FT CARBOHYD 343 343 N-linked (GlcNAc..)(Potential)
FT CARBOHYD 410 410 N-linked (GlcNAc..)(Potential)
SQ SEQUENCE 998 AA; 112096 MW; 479B9CA0D2BB06EB CRC64;

Query Match 96.8%; Score 3139; DB 1; Length 998;
Best Local Similarity 97.7%; Pred. No. 7.3e-227;
Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

QY 1 MVTQTRFPSPWIIICYYIWLGFATGAEQAQAEVLLDSKAQTELEWISSPSPGWERISG 60
Db 1 MVTQTRFPSPWIIICYYIWLGFATGAEQAQAEVLLDSKAQTELEWISSPSPGWERISG 60
QY 61 LDENYPIRIFYQVQVMEPNQNMWLTNWSISKNAQRIFEVLEKFTLDCNSLPGVLGTC 120
Db 61 LDENYPIRIFYQVQVMEPNQNMWLTNWSISKNAQRIFEVLEKFTLDCNSLPGVLGTC 120
QY 121 ETEENLYVEEDYDGTGRNIRENLVKIDTIADESFTQGDIGERRKMLNTEVREIGPLSK 180
Db 121 ETEENLYVEEDYDGTGRNIRENLVKIDTIADESFTQGDIGERRKMLNTEVREIGPLSK 180
QY 181 GFYLAFQDVACIALYSVKYYKKCWITVENLAVFPDTVGSEFSSLVEVRGTCVSSAAE 240
Db 181 GFYLAFQDVACIALYSVKYYKKCWITVENLAVFPDTVGSEFSSLVEVRGTCVSSAAE 240
QY 241 EAENSPPRMHCSAGEWLVPIGKICIKAGYQOKGDTCEPCRRRYKSSQTLQCSRCPH 300
Db 241 EAENSPPRMHCSAGEWLVPIGKICIKAGYQOKGDTCEPCRRRYKSSQTLQCSRCPH 300
QY 301 FSDREGSSRECEGDYRAPSDPEYVACTPSPAPQULNINQTYTSLFMSPADNGR 360
Db 301 FSDREGSSRECEGDYRAPSDPEYVACTPSPAPQULNINQTYTSLFMSPADNGR 360
QY 361 NDVTYRILCRGCSWEGECVPCSGNIGYMPQGTLEDNYTVMDLAAHAYTEVEAVNG 420
Db 361 NDVTYRILCRGCSWEGECVPCSGNIGYMPQGTLEDNYTVMDLAAHAYTEVEAVNG 420
QY 421 VSDLSRSQRLFAAVSITGQAAPSQVSGVKERVLQSRVLSQEPHPHCATTEYEIKY 480
Db 421 VSDLSRSQRLFAAVSITGQAAPSQVSGVKERVLQSRVLSQEPHPHCATTEYEIKY 480
QY 481 YEKDQRERTSTLKTSTASINNLKRGTYVYQIRAVTAGYGNYSFRLDVAITLERASG 540
Db 481 YEKDQRERTSTLKTSTASINNLKRGTYVYQIRAVTAGYGNYSFRLDVAITLERASG 540
QY 541 KMEEATVSSSEONPVIIIAVAVAGTIIIVFVFGFFGRRHCGYSKADCEGDELYFH 599
Db 541 KMEEATVSSSEONPVIIIAVAVAGTIIIVFVFGFIIIGRRHCGYSKADCEGDELYFH 599

RESULT 7
Q8C7N2 PRELIMINARY; PRT; 593 AA.
AC Q8C7N2;
DT 01-MAR-2003 (Tremblere1.23, Created)
DT 01-MAR-2003 (Tremblere1.23, Last sequence update)
DT 01-MAR-2004 (Tremblere1.26, Last annotation update)
DE Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched
DE library, clone: C6300306 product: Eph receptor A7, full insert
DE sequence.
GN Name=Epha7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10091;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;

```

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RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RA The FANTOM Consortium;
RT "The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohata E., Watahiki M.,
RA Oneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuyama S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:11757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Hippocampus;
RA Adachi U., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK049848; BAC33955.1; -.
DR HSSP; P54763; INUK.
DR MKD; MGI:95276; Epha7.
DR GO; GO:0005615; Extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR001090; Ephrin receptor.
DR InterPro; IPR003963; FcRII subd.
DR InterPro; IPR003961; FN-III.
DR InterPro; IPR008957; FN-III-like.
DR InterPro; IPR008979; Gal_bind-like.
DR InterPro; IPR001426; YKase receptorV.
DR Pfam; PF01404; Ephrin_Lbd_1.
DR Pfam; PF00041; fn3_1.
DR PRINTS; PR00014; FNTYPEIII.
DR ProDom; PD001495; Ephrin_receptor; 1.

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DR SMART; SM00615; Eph_1bd; 1.
 DR SMART; SM00600; FN3; 2.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS50853; FN3; 2.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 KW RECEPTOR.
 SQ SEQUENCE. 593 AA; 66324 MW; 119802525D73F3DB3 CRC64;

Query Match 96.4%; Score 3126; DB 2; Length 593;
 Best Local Similarity 99.7%; Pred. No. 3.3e-226;
 Matches 587; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVVQTRPSPWIIICYLMLGFHGTGEAQAQAKEVLLDLSKAQOTLEWISSPPSGMEETISG 60
 DB 1 MVVQTRPSPWIIICYLMLGFHGTGEAQAQAKEVLLDLSKAQOTLEWISSPPSGMEETISG 60
 QY 61 LDENVYTRIRYQVQVQVNEPNQNNMLRTNWSKGNAGRIFEVLEKTTLRDQNSLPVGLGTC 120
 DB 61 LDENVYTRIRYQVQVQVNEPNQNNMLRTNWSKGNAGRIFEVLEKTTLRDQNSLPVGLGTC 120
 QY 121 ETEFLYYEYEDYDGRNIRENLVYKIDTIADESFTQGDGERKMKTEVREIGPLSKK 180
 DB 121 ETEFLYYEYEDYDGRNIRENLVYKIDTIADESFTQGDGERKMKTEVREIGPLSKK 180
 QY 181 GFYLAPODVAGACIALVSKVYKKCWITIVENLAFFPDVTGSEFSSSLVEVAGTCVSSAEE 240
 DB 181 GFYLAPODVAGACIALVSKVYKKCWITIVENLAFFPDVTGSEFSSSLVEVAGTCVSSAEE 240
 QY 241 EAENSPPMHGSAEGEWLVPIGKCI CKAGYQOKGDTCEPCGRFYKSSSODLQCSRCTHS 300
 DB 241 EAENSPPMHGSAEGEWLVPIGKCI CKAGYQOKGDTCEPCGRFYKSSSODLQCSRCTHS 300
 QY 301 FSDDESGSRCECEGYRAPSDPRVYACTRPSPAPQNLFININTYLSLESPADNGR 360
 DB 301 FSDDESGSRCECEGYRAPSDPRVYACTRPSPAPQNLFININTYLSLESPADNGR 360
 QY 361 NDVTYRILCKRCMSWQECVPCGSNIGMPQOTGLENYVTVMLLAHANTFEVAVNG 420
 DB 361 NDVTYRILCKRCMSWQECVPCGSNIGMPQOTGLENYVTVMLLAHANTFEVAVNG 420
 QY 421 VSDLSRSQLPFAVSIITGQAPSOVSQVWKEKRVLOSVOISWQEPHPNGVITEYIKY 480
 DB 421 VSDLSRSQLPFAVSIITGQAPSOVSQVWKEKRVLOSVOISWQEPHPNGVITEYIKY 480
 QY 481 YENDQRRRTYSLTKSTSTASINNLKPGTYVFPRIYTAAGYGNVSPRLDVATLEASG 540
 DB 481 YENDQRRRTYSLTKSTSTASINNLKPGTYVFPRIYTAAGYGNVSPRLDVATLEASG 540
 QY 541 KMFPEATVSSSEONPVIIIAVAVAGTIIIVMVFGLIIRRHGYSRAD 589
 DB 541 KMFPEATVSSSEONPVIIIAVAVAGTIIIVMVFGLIIRRHGYSRAD 589

RESULT 8
 EPI7 CHICK STANDARD; PRT; 993 AA.
 ID EPI7 CHICK STANDARD; PRT; 993 AA.
 AC 062423;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ephrin type-A receptor 7 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor CEPHA7) (Tyrosine-protein kinase receptor CEK11).
 GN Name=EPAH7; Synonyms=CEK11;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 OC NCBI_TaxID=9031;
 RX NCBI_TaxID=9031;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 MDLLINE=98092111; PubMed=9431814; DOI=10.1016/S0925-4773(97)00147-0;

RA Araujo M., Nieto M.A.;
 RT "The expression of chick EphA7 during segmentation of the central and peripheral nervous system";
 RL Mech Dev. 68:173-177(1997).
 CC -1- FUNCTION: Receptor for members of the ephrin-A family.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Within the nervous system, expression is restricted to prosomeres 1 and 2 in the dienecephalon and all the rhombomeres in the hindbrain during segmentation stages. Later on, a superimposed pattern appears that correlates with the formation of several axonal tracts. In the somitic mesoderm, the expression correlates with segmentation and the guidance of both neural crest and motor axons through the sclerotomes.
 CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin receptor subfamily.
 CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; Y14271; CAA74643.1; -.
 DR HSBP; P54763; IJPA.
 DR InterPro; IPR006209; EGF like.
 DR InterPro; IPR001090; Ephrin receptor.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR008957; FN_III-like.
 DR InterPro; IPR003962; FNIII subd.
 DR InterPro; IPR008979; Gal bind like.
 DR InterPro; IPR009030; Grow fac recept.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR007719; Prot_kinase.
 DR InterPro; IPR001660; SAM.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase AS.
 DR InterPro; IPR001426; YKase receptorV.
 DR Pfam; PF01404; Ephrin_1bd; 1.
 DR Pfam; PF00041; FN3; 2.
 DR Pfam; PF00069; Kinase; 1.
 DR Pfam; PF00536; SAM; 1.
 DR PRINTS; PR00104; FNTYPEIII.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000145; Ephrin receptor; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00615; Eph_1bd; 1.
 DR SMART; SM00454; SAM; 1.
 DR SMART; SM00219; TYRK; 1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS50853; FN3; 2.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE; PS50105; SAM DOMAIN; 1.
 KM ATP-binding; Glycoprotein; Phosphorylation; Receptor; Repeat; Signal;
 KM Transferrase; Transmembrane; Tyrosine-protein kinase.
 FT SIGNAL 1 30
 FT CHAIN 31 993
 FT DOMAIN 31 551
 FT TRANSMEM 552 572
 FT DOMAIN 573 993
 FT DOMAIN 192 328
 FT DOMAIN 331 433
 FT DOMAIN 443 535
 FT DOMAIN type-III 1.
 FT Fibronectin type-III 2.

| | | | | |
|---------------------------|----------|---------|---------------------|---|
| FT | DOMAIN | 628 | 889 | Protein kinase. |
| FT | DOMAIN | 918 | 982 | SAM. |
| FT | SITE | 991 | 993 | PDZ-binding motif (Potential). |
| FT | NP_BIND | 634 | 642 | ATP (By similarity). |
| FT | DISULFID | 74 | 109 | By similarity. |
| FT | BINDING | 660 | 660 | ATP (By similarity). |
| FT | ACT_SITE | 753 | 753 | By similarity. |
| FT | MOD_RES | 603 | 603 | Phosphotyrosine (by autocatalysis) (Potential). |
| FT | MOD_RES | 609 | 609 | Phosphotyrosine (by autocatalysis) (Potential). |
| FT | MOD_RES | 786 | 786 | Phosphotyrosine (by autocatalysis) (Potential). |
| FT | MOD_RES | 935 | 935 | Phosphotyrosine (by autocatalysis) (Potential). |
| FT | CARBOHYD | 343 | 343 | N-linked (GlcNAc...) (Potential). |
| FT | CARBOHYD | 410 | 410 | N-linked (GlcNAc...) (Potential). |
| SO | SEQUENCE | 993 AA; | 111366 MW; | HECFF9603047605BD CRC64; |
| Query Match | | | | |
| Best Local Similarity | | 93.5%; | Score 1031.5; | DB 1; Length 993; |
| Matches 566; Conservative | | 17; | Pred. No. 8.7e-219; | Indels 5; Gaps 1 |

[illegible]

DE insert sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=99279253; PubMed=10349656; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RA The FANTOM Consortium,
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsuami T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imocani K., Ishii Y., Itoh M., Kaga I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohseki N., Okazaki Y.,
RA Saito R., Satoh K., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Saeki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK089143; BAC40764.1; -.
DR HSSP; P54763; INDX.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005003; F:ephrin receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007159; P:transmembrane receptor protein tyrosine kin. .; IEA

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DR InterPro: IPR006209; EGF like.
DR InterPro: IPR001090; Ephrin_receptor.
DR InterPro: IPR003962; FcIII subd.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR008979; Gal_bind like.
DR InterPro: IPR009030; Grow_fac_recept.
DR InterPro: IPR001426; YKase_receptor.
DR Pfam: PF00404; Ephrin_lbd; 1.
DR Pfam: PF00041; fn3; 2.
DR PRINTS: PR00014; FNTYPEIII.
DR ProDom: PD001495; Ephrin_receptor; 1.
DR SMART: SM00615; EPH_lbd; 1.
DR SMART: SM00060; FN3_2.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00853; FN3; 2.
DR PROSITE: PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR KEGG: K00000; Receptor.
SQ SEQUENCE 681 AA; 75336 MW; 92B9187AB78BE722 CRC64;

Query Match 57.4%; Score 1862.5; DB 2; Length 681;
Best Local Similarity 56.6%; Pred. No. 3.9e-131;
Matches 351; Conservative 98; Mismatches 136; Indels 35; Gaps 9;

6 RFPSEWILCY-----IM-----LLGFAHTEQAQAKVLLDLSKAQOETELEMISPPSG 54
25 RVPASLACGSAAPLKGPIMLTCLICALRTILASPSNEVNLDSRTVMGDMIAFPKNG 84
55 WEISGLDENTYPTIRYQVCVMEPNQNNMLRTNWSKGNQRIFFVELKFTLRDQNSLPG 114
85 WEISGEVDENYAPLHTYQVCVMEQNNMLRTNWSISGASRIFFELKFTLRDQNSLPG 144
115 VLGTCKETFNLYYETDYDGRNIRENLYKIDITIADESTQGLGERKKAKNTREYREI 174
145 GLGTCKETFNMYYESPDENGRSISENOYKIDITIADESTFELDGRVKKAKNTREYADV 204
175 GPLSKGPFYLAFOVGACIALVSVKVVYKKCMITVENAVPDTVSEPSLVEVGTG 234
205 GPLSKGPFYLAFOVGACIALVSVKVVYKKCMITVENAVPDTVSEPSLVEVGTG 264
235 VSSAEBAENSPRMCSAEGEMLVPIGKICAGYQOQKGTCEPCGRFRYKSSQDLQCS 294
265 VN--HSTVDDBPRKMGSAEGEMLVPIGKICAGYQOQKGTCEPCGRFRYKSSQDLQCS 322
295 RCPHSPSDBRSGRCECEDGYRAPSDPYVACTRPPSPADNLIENINQTVSLEWSP 354
323 KCPHSPHTEBASSTSCVCEKDYFRKSDPPPTMACTRPPSPADNLIENINQTVSLEWIP 382
355 ADNGGRDVTYRILCKKCSWQEGCVPCGSNIGVMPOOTGEDVYVVMMDLAHANTFE 414
383 ADTGGRDVTYRILCKKCSWQEGCVPCGSNIGVMPOOTGEDVYVVMMDLAHANTFE 442
415 VEAANGVSDLSRQSLFAVAISITGQAAPSOVSGVMEKERVQSRVQSLSMQEPHPNGVIT 474
443 IEAANGVSDLSRQSLFAVAISITGQAAPSOVSGVMEKERVQSRVQSLSMQEPHPNGVIT 502
475 EYEIKYKQDRETYSTLTKTSTASINNIKPGTVYFOIRAVTAAGYNGVSPRLDVAT 534
503 EYEIKYKQDRETYSTLTKTSTASINNIKPGTVYFOIRAVTAAGYNGVSPRLDVAT 558
535 LEBSAGMFEAT-----AVSSEONPVIIAAYAVAGTIIIVMVGFIIGRHCHGYKXDO 590
559 -----FETTPVSVASNDOSQPIIAVSVTVGVILLAVMI-GPILSGRRCGISYAKQ 609
591 EGDEE-LYFSLVTNHLSTV 609
610 DPBEKMHF-----NGHIKL 625

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AC P54757;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ephrin type-A receptor 5 precursor (EC 2.7.1.112) (Tyrosine-protein
DE kinase receptor EHK-1) (EPH homology kinase-1).
GN Name=EphA5; Synonyms=Ehk-1, Ekhl,
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4 AND 5).
RP STRAIN=Sprague-Dawley; TISSUE=Brain;
RC MEDLINE=94067777; PubMed=7504232;
RA Maisondiere P.C., Barrezaeta N.X., Yancopoulos G.D.;
RT "Ehk-1 and Ehk-2: two novel members of the Ehn receptor-like tyrosine
RT kinase family with distinctive structures and neuronal expression.";
RL Oncogene 8:3277-3288(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 6).
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=95206467; PubMed=7896466; DOI=10.1016/0306-4522(94)90014-0;
RA Taylor V., Miescher G.C., Pfaffr S., Honegger P., Breitschopf H.,
RA Laessmann H., Steck A.J.;
RT "Expression and developmental regulation of Ehk-1, a neuronal Elk-like
RT receptor tyrosine kinase in brain.";
RL Neuroscience 63:163-178(1994).
CC -1- FUNCTION: Receptor for members of the ephrin-A family. Binds to
CC ephrin-A1, -A2, -A3, -A4 and -A5.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=6;
CC Name=1;
CC IsoId=P54757-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P54757-2; Sequence=VSP_003001;
CC Name=3;
CC IsoId=P54757-3; Sequence=VSP_003002;
CC Name=4;
CC IsoId=P54757-4; Sequence=VSP_003002, VSP_003003;
CC Name=5;
CC IsoId=P54757-5; Sequence=VSP_003001, VSP_003002, VSP_003003;
CC Name=6;
CC IsoId=P54757-6; Sequence=VSP_003000, VSP_003002;
CC -1- TISSUE SPECIFICITY: Almost exclusively expressed in the nervous
CC system. Predominantly expressed in neurons.
CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin
CC receptor subfamily.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
CC -----
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CC -----
DR EMBL: X78689; CA55357.1; -.
DR PIR: S49015; S49015.
DR PIR: S51603; S51603.
DR HSSP: P54763; 1UPA.
DR InterPro: IPR006209; EGF like.
DR InterPro: IPR001090; Ephrin_receptor.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR008957; FN_III-like.
DR InterPro: IPR008979; Gal_bind like.
DR InterPro: IPR009030; Grow_fac_recept.

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DR InterPro: IPR011039; Kinase_like.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR001650; SAM.
 DR InterPro: IPR001245; Tyr_kinase.
 DR InterPro: IPR008265; Tyr_kinase_AS.
 DR InterPro: IPR001425; YKase_receptorV.
 DR Pfam: PF01404; Ephrin_1bd; 1.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00069; Pkinase; 1.
 DR Pfam: PF00536; SAM; 1.
 DR PRINTS: PR00014; ENTPELII.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD001495; Ephrin_receptor; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00615; Eph_1bd; 1.
 DR SMART: SM00219; Tyrc; 1.
 DR PROSITE: PS01166; EGF_2; UNKNOWN_1.
 DR PROSITE: PSS0853; FN3; 2.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 DR PROSITE: PSS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00799; RECEPTOR_TYR_KIN_V_1; 1.
 DR PROSITE: PS00791; RECEPTOR_TYR_KIN_V_2; 1.
 DR PROSITE: PSS0105; SAM_DOMAIN; 1.
 KW Alternative splicing; ATP-binding; Glycoprotein; Phosphorylation;
 KW Receptor; Repeat; Signal; Transmembrane;
 KW Tyrosine-protein kinase.
 FT CHAIN 1 26
 FT DOMAIN 27 1005
 FT TRANSMEM 27 575
 FT DOMAIN 576 596
 FT DOMAIN 597 1005
 FT DOMAIN 222 356
 FT DOMAIN 359 461
 FT DOMAIN 471 561
 FT DOMAIN 677 938
 FT DOMAIN 967 1005
 FT NP_BIND 683 691
 FT BINDING 709 709
 FT ACT_SITE 802 802
 FT MOD_RES 652 652
 FT MOD_RES 658 658
 FT MOD_RES 835 835
 FT MOD_RES 984 984
 FT CARBOHYD 266 266
 FT CARBOHYD 301 301
 FT CARBOHYD 371 371
 FT CARBOHYD 425 425
 FT CARBOHYD 438 438
 FT CARBOHYD 463 463
 FT VARSPLIC 10 20
 FT VARSPLIC 306 357
 FT VARSPLIC 358 470
 FT VARSPLIC 597 621
 FT CONFLICT 170 170
 FT CONFLICT 566 566

By similarity.
 Ephrin type-A receptor 5.
 Extracellular (Potential).
 Potential.
 Cytoplasmic (Potential).
 Cys-rich.
 Fibronectin type-III 1.
 Fibronectin type-III 2.
 Protein kinase.
 SAM.
 ATP (By similarity).
 ATP (By similarity).
 By similarity.
 Phosphotyrosine (by autocatalysis) (By similarity).
 Phosphotyrosine (by autocatalysis) (Potential).
 Phosphotyrosine (by autocatalysis) (By similarity).
 N-linked (GlcNAc. . .) (Potential).
 N-linked (GlcNAc. . .) (Potential).
 N-linked (GlcNAc. . .) (Potential).
 N-linked (GlcNAc. . .) (Potential).
 N-linked (GlcNAc. . .) (Potential).
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 N-linked (GlcNAc. . .) (Potential).
 GRRRTGGRGG -> DADGPRADSWCHAF (in isoform 6).
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 VCRPGFKAQSPHSGKCPHSTYHBEATSCVCEKDYR
 RESDPRMACT -> G (in isoform 2 and isoform 5).
 /FtId=VSP_003001.
 RPPAPRNALSNVETSPLEWIPPADYCGKDVSYILCK
 KCHSHAGVCEGCHVYLPQOLGLKNTSYMDPLAHITY
 TPEIEAVNGVSDLSPTGROYVNVVITNOA -> T (in isoform 3, isoform 4, isoform 5 and isoform 6).
 /FtId=VSP_003002.
 SGSCCEGCRASLCAVHPSLIW -> F (in isoform 4 and isoform 5).
 /FtId=VSP_003003.
 D -> E (in Ref. 2).
 G -> A (in Ref. 2).

FT CONFLICT 578 578 G -> A (in Ref. 2).
 FT CONFLICT 669 669 G -> A (in Ref. 2).
 FT CONFLICT 708 708 T -> I (in Ref. 2).
 FT CONFLICT 979 979 T -> I (in Ref. 2).
 SQ SEQUENCE 1005 AA, 111007 MW, 1AED42C99693C574 CRC64;
 Query Match 56.2%; Score 1821; DB 1; Length 1005;
 Best Local Similarity 54.6%; Pred. No. 8, 8e-128;
 Matches 350; Conservative 97; Mismatches 138; Indels 56; Gaps 11;
 QY 6 RPPSWIILCY-----IW-----LGFATGGEAQAQAEVLLDSKQOTELEMISSPPG 54
 DB 25 RVPASLAGCTSAKLPKPLWTCLLCALRTLLASPSENVLLDSRVVLGDLGIAPPKXG 84
 QY 55 WEISGLDENYPTIRTYOVCOVMEPNQNMRLTNMISKNAQRIFVELKFTLADCSLP 114
 DB 85 WEIEGVDEYNAPITHTYYQCKWEGQNMWLLTWSINSGASRIFELKFTLADCSLP 144
 QY 115 VLGTCKETPLYYEEDYDTGRNIRENLVKIDTLADSSFTQGLGERKMKLNTVEVREI 174
 DB 145 GLGTCKETPLMYFEESDDEGRNIRKIDTLADSSFTQGLGERKMKLNTVEVREI 204
 QY 175 GPLSKGFYLAPODVACIALVSVKYYKKCWITVENLAVFPPTVYGFSESSLVEVRCG 234
 DB 205 GPLSKGFYLAPODVACIALVSVRYKKCSVNHHLAVFPPTITGADSSQLIEVSGSC 264
 QY 235 VSSAEBAENSPPRMHCSAGEMLVPIGKICRAGYQOQKDYCEPCGRFRYKSSODLQCS 294
 DB 265 VN--HSVTDDPPRMHCSAGEMLVPIGKCMCRAGYEEKNGTCQVCRPGFFKASPHSOTCS 322
 QY 295 RCTHFSFDSREGSRECEDEGYRRASDPYVACTRPSPAPQNLININQTTYSLEWSP 354
 DB 323 KCPHSTYHBEASTSCVCEKDYFRRESDEPTACTRPAPRAVSNVNETSPLEWIP 382
 QY 355 ADNGANDTYRILCKRCSWEGECVPCGNSGYMPQGTLENNYTVMDLAAHYTFE 414
 DB 383 ADTGAGKDVSYILCKCKNSHACVCECGHRYLPQOLGLKNTSYMDPLAHITYFE 442
 QY 415 VEAVNGVSDLSRSQRLFAAVSITTGAPSOVSGVKEKRVLORSVOLSNQEPHNGVIT 474
 DB 443 IEAVNGVSDLSPTGRYVSNVTNQAPSPVTNVKGIKAKSISLSNQEPDRPGIIL 502
 QY 475 EYIKIYKEDQERRTSTLTKYSTASINNLKPGTYVYQIARVTAAGGNVSPRLDVAT 534
 DB 503 EYIKIYKEDQ-ETSYTIKSKETITTAGLKPAASYVQIARVTAAGVGFSPRPE--- 558
 QY 535 LBEASGKMEFATV---SSEQNPVITIAVAVAGTIIIVEMVGFII-----GRR- 581
 DB 559 -----FETTVFPGASNDQSQIPITIGSVYVGVILLAVMI-GFILSGSCCEGCRAS 609
 QY 582 -----HGGYSKADQEGDEE-LYFHSLVNTNHLVS 609
 DB 610 SLCAVAHPSLIWRCGYSKAKQDPEEEKMHFH-----NGHIKL 646
 RESULT 11
 ID EPAS HUMAN STANDARD; PRT; 1037 AA.
 AC P54756;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ephrin type-A receptor 5 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor HK-1) (Eph homology kinase-1) (Receptor protein-tyrosine kinase HEK7).
 DE Name=EPAS; Synonyms=BHL, HEK7;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;

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RA  Miescher G.C.;
RP  SEQUENCE OF 25-1037 FROM N.A.
RN  [2]
RC  TISSUE=Brain;
RX  MEDLINE=95206782; PubMed=7698931;
RA  Fox G.M., Holst P.L., Chute H.T., Lindberg R.A., Janssen A.M.,
RA  Baas R., Welcher A.A.;
RT  "cDNA cloning and tissue distribution of five human EPH-like receptor
RT  protein-tyrosine kinases.";
RL  Oncogene 10:897-905(1995).
CC  -1- FUNCTION: Receptor for members of the ephrin-A family. Binds to
CC  ephrin-A1, -A2, -A3, -A4 and -A5.
CC  -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC  tyrosine phosphate.
CC  -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC  -1- ALTERNATIVE PRODUCTS:
CC  Event=Alternative splicing; Named isoforms=2;
CC  Comment=Additional isoforms seen to exist;
CC  Name=1;
CC  IsoId=P54756-1; Sequence=Displayed;
CC  Name=2;
CC  IsoId=P54756-2; Sequence=VSP_00299;
CC  -1- TISSUE SPECIFICITY: Almost exclusively expressed in the nervous
CC  system.
CC  -1- SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin
CC  receptor subfamily.
CC  -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC  -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; X95425; CAA64700.1; -.
DR  EMBL; U36644; AAA74245.1; -.
DR  HSSP; P54763; 1JPA.
DR  Genew; HGNC:3389; EPHAS.
DR  MIM; 600004; -.
DR  GO; GO:0016021; C:integral to membrane; TAS.
DR  GO; GO:0005005; F:transmembrane-ephrin receptor activity; TAS.
DR  GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR  InterPro; IPR006209; EGF_like.
DR  InterPro; IPR001090; Ephrin_receptor.
DR  InterPro; IPR003961; FN_III.
DR  InterPro; IPR008957; FN_III-like.
DR  InterPro; IPR003962; FNIII_sub.
DR  InterPro; IPR008979; Gal_bind_like.
DR  InterPro; IPR009030; Grow_fac_recept.
DR  InterPro; IPR010009; Kinase_like.
DR  InterPro; IPR007019; Prot_kinase.
DR  InterPro; IPR001660; SAM.
DR  InterPro; IPR001245; Tyr_kinase.
DR  InterPro; IPR008266; Tyr_kinase_AS.
DR  InterPro; IPR001426; Ykase_receptorV.
DR  Pfam; PF01404; Ephrin_lbd; 1.
DR  Pfam; PF00041; fn3; 2.
DR  Pfam; PF00069; Kinase; 1.
DR  Pfam; PF00536; SAM; 1.
DR  PRINTS; PR00014; ENTYPETII.
DR  PRINTS; PR00109; TYRKINASE.
DR  ProDom; PD001495; Ephrin_receptor; 1.
DR  ProDom; PD000001; Prot_kinase; 1.
DR  SMART; SM00615; EPH_lbd; 1.
DR  SMART; SM00060; FN3_2.
DR  SMART; SM00454; SAM; 1.
DR  SMART; SM00219; Tyrc; 1.
DR  PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR  PROSITE; PS00853; FN3; 2.

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| DR | PROSITE; PS00107; PROTEIN KINASE ATP. 1. |
| DR | PROSITE; PS00011; PROTEIN_KINASE_DOM. 1. |
| DR | PROSITE; PS00109; PROTEIN_KINASE_TYR. 1. |
| DR | PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1. |
| DR | PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1. |
| DR | PROSITE; PS0105; SAM_DOMAIN. 1. |
| KM | Alternative splicing; ATP-binding; Glycoprotein; Phosphorylation; |
| KW | Receptor; Repeat; Signal; Transferase; Transmembrane; |
| KM | Tyrosine-protein kinase. |
| FT | SIGNAL 1 24 Potential. |
| FT | CHAIN 25 1037 Ephrin type-A receptor 5. |
| FT | DOMAIN 25 573 Extracellular (Potential). |
| FT | TRANSNM 574 594 Potential. |
| FT | DOMAIN 595 1037 Cytoplasmic (Potential). |
| FT | DOMAIN 220 354 Cys-rich. |
| FT | DOMAIN 357 459 Fibronectin type-III 1. |
| FT | DOMAIN 469 559 Fibronectin type-III 2. |
| FT | DOMAIN 675 936 Protein kinase. |
| FT | DOMAIN 965 1029 SAM. |
| FT | SITE 1035 1037 PDZ-binding motif (Potential). |
| FT | NP_BIND 681 689 ATP (By similarity). |
| FT | BINDING 707 707 ATP (By similarity). |
| FT | ACT_SITE 800 800 By similarity. |
| FT | MOD_RES 650 650 Phosphotyrosine (by autocatalysis) (By similarity). |
| FT | MOD_RES 656 656 Phosphotyrosine (by autocatalysis) (By similarity). |
| FT | MOD_RES 833 833 Phosphotyrosine (by autocatalysis) (Potential). |
| FT | MOD_RES 982 982 Phosphotyrosine (by autocatalysis) (By similarity). |
| FT | CARBOHYD 264 264 N-linked (GlcNAc . . .) (Potential). |
| FT | CARBOHYD 299 299 N-linked (GlcNAc . . .) (Potential). |
| FT | CARBOHYD 369 369 N-linked (GlcNAc . . .) (Potential). |
| FT | CARBOHYD 423 423 N-linked (GlcNAc . . .) (Potential). |
| FT | CARBOHYD 436 436 N-linked (GlcNAc . . .) (Potential). |
| FT | CARBOHYD 461 461 N-linked (GlcNAc . . .) (Potential). |
| FT | VARSPLIC 597 619 SCSCGGGRASSLCAVAHPILIW -> R (in isoform 2). |
| SEQUENCE | 1037 AA; 114784 MW; FCAC4FC95AFAF8699 CR664; /FtId=VSP_002999. |
| Query Match | Best Local Similarity 56.1%; Score 1819; DB 1; Length 1037; |
| Matches | 348; Conservative 98; Mismatches 134; Indels 52; Gaps 11; |
| OY | 6 RFPSW--IILCYTLWGFAHTGEAOAAKEVILLDSKAQOETLEWISSPPSGMEISGLIDE 63 |
| DB | 37 RAPIMTCLILC-----ALRTILASPENSEVELDLSTRVMGDLGIWAEPKXMGMEIGEVDE 91 |
| OY | 64 NYEPIRTYYGVOWNEPNNMMRLRTNWSKGNAORIIPBLKPTLADCNLSLPGLTGCKETF 123 |
| DB | 92 NYAPIHIYQVCWVEQNQNNMLLTSMNSBEGASIFIEFKTLTLDNCNLSPLGLTGCKETF 151 |
| OY | 124 NLVYEETDYDTGNRIRENLVYKIDITIADESFTGDGGERMKAKNTVEAREISGPSSKGFY 183 |
| DB | 152 NMVFESDDQNGRIKENQYIKIDITIAADESFTELDDGRMKAKNTVEARDVGSLSKGFY 211 |
| OY | 184 LAPDVAGACIALVSVKVYKKCWTVLENLAVFPDTVTGSSEFFSLVEVRGTCVSSAAEBEA 243 |
| DB | 212 LAFODVAGACIALVSVRYKKCPVSRVHLLAVFPDTITGADSOLLLEVSGSCVN--HSVTD 269 |
| OY | 244 NSPMHGSABEMVLVPFGKCI CKRGYQOKDTCGPCRRPFYKSSSODLCRCRCTHSPSD 303 |
| DB | 270 EPPMHGSABEMVLVPFGKCMCKCKAYEEKNGTCCVCGPRFFKASPHIQSCCKCPHSHYTH 329 |
| OY | 304 REGSSRCECEDGYRASDPFYVACTPPSAPOULININQITVYSLEMSPADNGCHANDV 363 |
| DB | 330 EEAISTCVCEEDYVRRRESDEPTMACTRPPAPRAAISVANMETSYFLFMIRPADTGCRKD V 389 |
| OY | 364 TYRILCRCSWEQECVPCGSNIGMYDMQQTGLENDVYTMDDLAAHANYTEVEAVNGVSD 423 |
| DB | 390 SYTAACKCKNSHGVCCECGGHVYLIRPGSLKKTYSVMVDLLAHNTYTEIEAVNGVSD 449 |


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Db      5 LSIIVLLGCCVLSGSGELSPQSPNEVNLDSKTIQGEIWMISYPSHGHEEISGVDEHYTP 64
Qy      68 IRTYOVCGMEPNPNMNLRTNWSISGNQRIFVELKFTLRCONSLPGVLGTCKEENLY 127
Db      65 IRTYOVCGMHSQNMHLRTMWPSPNSHOKIYVELKFTLRCONSLPLVLGTCKEETFNLY 124
Qy      128 YETDYDTGRNIRENLVYKIDITIAADESFTQDGLGRKKKLNTVEVEIGLPSKKGFLAFQ 187
Db      125 MESDDHGVKREHQFTKIDITIAADESFTQDGLGRKKKLNTVEVEIGLPSKKGFLAFQ 184
Qy      188 DVGACIALVSKYTKYKKWTIVENLAVPDTVTGSESLYEVNCTCYSAABEAEANSPR 247
Db      185 DVGACIALVSKYTKYKKWTIVENLAVPDTVTGSESLYEVNCTCYSAABEAEANSPR 241
Qy      248 MHGSAEGEVLPIGKCTCKAGYQKGDTCCEPGRFRFYSSQDDIQCSRCPHSPSDEG 307
Db      242 MYCTGEGMLVPIGKCTCKAGYQKGDTCCEPGRFRFYSSQDDIQCSRCPHSPSDEG 301
Qy      308 SRCEEDGYRAPSDPPYVACTRPPSAPQNLIFNIQTTSLEWSPPADNGGRNDVTYRI 367
Db      302 MNGCENNYFPAEADPPSMACTRPPSAPRNVISINETSILDMSPWLDGTGRKDITFNI 361
Qy      368 LCRKCSMEQGEVPCGSNIGMPQQTGLEDNVYTVMDLILANTFEVEAVNGVSDLSRS 427
Db      362 ICKKCGMNVRCCEPSPVRFPLQGLTNTVTVDLANTFYFIDAVNGVSELSSP 421
Qy      428 ORLPAVSIITGOAPSOVSGVMKERVLRQSVOLSMOEBEPHNPVITFEYIKYKQORE 487
Db      422 PROPAVASITNQAPSPVMITKDRISRSISLSMOEPHPNGIILDEYKYEKQOE 481
Qy      488 RTVSTLTKSTASINNLKPGTVVYFOIRAVTAGYGNYSPLDVALTEASGKMFEXTA 547
Db      482 TSYTILARGNVTISSLKPDITYVFOIRARATAGYGNYSKFEFETSP-----DSFS 534
Qy      548 VSSSQNPVITIAVAVAGTITLVFMVEGFTIGRHCGYSKADQGDDEE-LYFHSLLVNEH 606
Db      535 ISGNSHVMIAMIAAVALIIVLT--VTVYVLVGRFCGYHKSMSAEKRLHF---GNCH 588
Qy      607 LSV 609
Db      589 LKL 591

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RT      expressed."
RL      Oncogene 8:1807-1813(1993).
CC      -1- FUNCTION: Receptor for members of the ephrin-A family. Binds to
CC      ephrin-A1, -A2, -A3, -A4 and -A5. Able to collapse growth cones.
CC      -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC      tyrosine phosphate.
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=3;
CC      Comment=Additional isoforms seem to exist;
CC      Name=3;
CC      IsoId=P54755-1; Sequence=Displayed;
CC      Name=1;
CC      IsoId=P54755-2; Sequence=VSP_003005;
CC      Name=2;
CC      IsoId=P54755-3; Sequence=VSP_003004, VSP_003005;
CC      -1- TISSUE SPECIFICITY: Detected in the 10-day embryonic brain, weaker
CC      expression in the rest of the 10-day embryo. Undetected in adult
CC      tissues.
CC      -1- SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin
CC      receptor subfamily.
CC      -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
CC      -1- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
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CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U03910; AAB60613.1; -.
DR      EMBL; U03910; AAB60612.1; -.
DR      EMBL; Z19058; CAA79508.1; -.
DR      PIR; I50615; I50615.
DR      HSP; P54763; IUPA.
DR      InterPro; IPR006209; BGF like.
DR      InterPro; IPR001090; Ephrin_receptor.
DR      InterPro; IPR003961; FN_III.
DR      InterPro; IPR008957; FN_III-like.
DR      InterPro; IPR003962; FNIII subd.
DR      InterPro; IPR008979; Gal bind like.
DR      InterPro; IPR009030; Grow_fac_recept.
DR      InterPro; IPR011009; kinase like.
DR      InterPro; IPR007019; Prot_kinase.
DR      InterPro; IPR001660; SAM.
DR      InterPro; IPR001245; Tyr_kinase.
DR      InterPro; IPR008266; Tyr_kinase_AS.
DR      InterPro; IPR001426; Ykase_receptorV.
DR      Pfam; PF01404; Ephrin_Ibd; 1.
DR      Pfam; PF00041; Fn3; 2.
DR      Pfam; PF00069; Kinase; 1.
DR      Pfam; PF00536; SAM; 1.
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DR      PRINTS; PR00109; TYRKINASE.
DR      ProDom; PD001495; Ephrin_Receptor; 1.
DR      ProDom; PD000001; Prot_kinase; 1.
DR      SMART; SM00615; EPH_Ibd; 1.
DR      SMART; SM00606; FN3; 2.
DR      SMART; SM00454; SAM; 1.
DR      SMART; SM00219; TYRK; 1.
DR      PROSITE; PS01186; BGF_2; UNKNOWN_1.
DR      PROSITE; PS00853; FN3; 2.
DR      PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR      PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
DR      PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR      PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR      PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR      PROSITE; PS01005; SAM_DOMAIN; 1.
DR      Alternatve splicing; ATP-binding; Glycoprotein; Phosphorylation;
DR      Receptor; Repeat; Signal; Transferrase; Transmembrane;
KW

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KW Tyrosine-protein kinase.
FT SIGNAL 1 31
FT CHAIN 32 1013
FT DOMAIN 32 549
FT TRANSMEM 550 570
FT DOMAIN 571 1013
FT DOMAIN 196 330
FT DOMAIN 333 435
FT DOMAIN 445 535
FT DOMAIN 651 912
FT DOMAIN 941 1013
FT SITE 1011 1013
FT NP_BIND 657 665
FT BINDING 683 683
FT ACT_SITE 776 776
FT MOD_RES 626 626
FT MOD_RES 632 632
FT MOD_RES 809 809
FT MOD_RES 958 958
FT CARBOHYD 240 240
FT CARBOHYD 275 275
FT CARBOHYD 345 345
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FT CARBOHYD 412 412
FT CARBOHYD 437 437
FT VARSPIC 280 443
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FT CONFLICT 981 1013
FT SEQUENCE 1013 AA; 112245 MM; AC36FDAEBF38382 CRC64;

Query Match 55.6%; Score 1802; DB 1; Length 1013;
Best Local Similarity 55.3%; Pred. No. 2,4e-126;
Matches 347; Conservative 96; Mismatches 137; Indels 48; Gaps 10;

8 PSM--IILCYIMLGFAHTEBAQAAYVLLDSKAQTELEWISSPPSGMEISGLDENTY 65
15 PGMTCCLLCALRSLLASPG----SEVNLLDSRTWGDGMLAYPKNGKEBGEVDENTY 69
66 TPARTYOVCOVMEPNONNMLRTNWKISKGNQRIFFELKFTLPDONSIPGLGCKEFTNL 125
70 APHTHYOVCKVMEQONNNMLLTWISNKGPPASSFELKFTLPDONSIPGLGCKEFTNM 129
126 YYVETDYTGRTNREMLYKIDITTADESFTQDGLGERKMKLNTVEAIEIPLSKKGFYLA 185
130 YPFESDEDEGRNIRENGYIKIDITTADESFTELDGLGRVKNKLTVEAVDVCPLTKKGFYLA 189
186 FOVVGACIALVSKYVKKKMTIVENLAVPDDVTYGESESLYEVKGTCS-SAAEAEEN 244
190 FOVVGACIALVSKYVKKKMTIVENLAVPDDVTYGESESLYEVKGTCS-SAAEAEEN 247
245 SPMHSGAGEMWLVPICGKICRAGYQOKGPTCEFCGRGFRKSSQDQGCRCPTHSSDR 304
248 -PMMHSGAGEMWLVPICGKICRAGYQOKGPTCEFCGRGFRKSSQDQGCRCPTHSSDR 306
305 EGSSRCECEDGYRAPSDPPVACTRPPSAPONLIFNINQTTVSLSEWSPADNGRNDVT 364
307 EASTSGCEHYFRRESDDPTMACTRPSPASISVNETSVLEWIPFADVGRKDV 366
365 YRLCKRCGSEWEGECVCGSNIGMPQGTGLIEDNYTVMLLAHANTTFVEAVNGVSD 424
367 YYLACKCKNSHSGCEACGSHVRLPQGTGKNTSVMMVMDLHNTTFFIEAVNGVSD 426
425 SRSQRLPAAVSIITGGAAPSOVGVKMKRYLORSVOLSWOEPHNPVITREYELIKYKED 484
427 NPGARQFVSVNVTINQAAAPSPVSSVKKGIITKNSISLSWQEPDPFNCIILIEYELIKFEKD 486

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QY 485 QERETVSTLTKTSASINNLKPGTYVYQIRAVTAAGYGNVSPRLDVALTEBASGMFE 544
DB 487 Q-ETSYTIIRKSKETATLADLKFSGSAVVFQIRARTAGYGFRRREFET-----SP 537
QY 545 ATAVSEQNPFVILAVNVAAGTIIIVPMVPGFIIGR-----H 582
DB 538 VLAASDQSQIPIT-VSVTVGVILLAVIGFLLSGCCDHGCGMASLRAVAYPSLIWR 596
QY 583 CGYSKADQEGDEE-LYFHSILVTEHLSV 609
DB 597 CGYSKAKQDEERKMFH----NGHILK 620

RESULT 14
ID EP33 HUMAN STANDARD; PRT; 983 AA.
AC P29330; Q9H2V3; Q9H2V4;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ephrin type-A receptor 3 precursor (EC 2.7.1.112) (Tyrosine-protein
DE kinase receptor ETK1) (HEK) (HEK4).
GN Name=EP33; Synonyms=ETK, ETK1, HEK,
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=92179233; PubMed=1311845;
RA Wicks I.P., Wilkinson D., Salvaris E., Boyd A.W.;
RT "Molecular cloning of HEK, the gene encoding a receptor tyrosine
RT kinase expressed by human lymphoid tumor cell lines.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:1611-1615 (1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Melanoma;
RX MEDLINE=20441582; PubMed=10987298;
RA Chiari R., Hames G., Stroobant V., Texter C., Maille B., Boon T.,
RA Coulie P.G.;
RT "Identification of a tumor-specific shared antigen derived from an Eph
RT receptor and presented to CD4 T cells on HLA class II molecules.";
RL Cancer Res. 60:4855-4863 (2000).
RN [3]
RP SEQUENCE OF 21-29 AND 840-860, AND CHARACTERIZATION.
RX MEDLINE=92147681; PubMed=1737782;
RA Boyd A.W., Ward L.D., Wicks I.P., Simpson R.J., Salvaris E., Wilks A.,
RA Welch K., Loudovaris M., Rockman S., Bushman I.;
RT "Isolation and characterization of a novel receptor-type protein
RT tyrosine kinase (hek) from a human pre-B cell line.";
RL J. Biol. Chem. 267:3262-3267 (1992).
RN [4]
RP SPLICED ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).
RX PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
RA Hillman R.T., Green R.E., Brenner S.E.;
RT "An unappreciated role for RNA surveillance.";
RL Genome Biol. 5:RESEARCH008.1-RESEARCH008.16 (2004).
CC -!- FUNCTION: Receptor for members of the ephrin-A family. Binds to
CC ephrin-A2, -A3, -A4 and -A5. Could play a role in lymphoid
CC function.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).
CC -!- SECRETED (isoform 2).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P29330-1; Sequence=Displayed;
CC Note=May be produced at very low levels due to a premature stop
CC codon in the mRNA, leading to nonsense-mediated mRNA decay;
CC Name=2;
CC IsoId=P29330-2; Sequence=VSP_002995, VSP_002996;

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[illegible]

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derje J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang Y., Hsieh F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stelphton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Pierce C.,
RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mulhany S.J.,
RA Roark S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunatrarre P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Schmech A., Schein J.E.,
RA Jones S.U., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity) .
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin
CC receptor subfamily.
CC EMBL; BC063282; AAH63282.1; .
DR HSSP; P54763.1; IKGy.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005503; F:ephrin receptor activity; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . ; IEA
DR InterPro; IPR006209; EGF_lke.
DR InterPro; IPR001090; Ephrin_receptor.
DR InterPro; IPR003962; FntII_subd.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR008979; Gal_bind_lke.
DR InterPro; IPR011009; Kinase_lke.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001660; SAM.
DR InterPro; IPR011510; SAM_2.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR InterPro; IPR001426; YKase_receptor.
DR Pfam; PF01404; Ephrin_lbd; 1.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF07647; SAM_2; 1.
DR PRINTS; PR00014; FNTPEP11.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD001495; Tyrokin receptor; 1.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00615; Eph_lbd; 1.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00454; SAM; 1.
DR SMART; SM00220; S_TKC; 1.

DR SMART; SMO0219; TYRKC; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50853; EN3; 2.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
DR PROSITE; PS50195; SAM_DOMAIN; 1.
KM ATP-binding; Glycoprotein; kinase; phosphorylation; Receptor;
KM transmembrane; transmembrane; tyrosine-protein kinase
SQ SEQUENCE 963 AA; 110160 MW; 1EBDABFC59282527 CRC64;

| Query Match | 55.5% | Score 1799 | DB 2 | Length 983 |
|-----------------------|------------------|---|-----------|------------|
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| Matches 332 | Conservative 103 | Mismatch 131 | Indels 16 | Gaps 6 |
| QY | 28 | QAAKEVLLDSKAQOOLEWISSPPSGWEELISGLDENTPRTRYQVCQVMEPNQNNMRT | 87 | |
| DB | 25 | QPSNHEVNLDSKTIQGLGCMISTYPSHGHEELISGVDEHTPRTRYQVCVMDHSSQNNMRT | 84 | |
| QY | 88 | NWISKNAQRIFEVLKFTLRDCNSLPGVLTGCKETFNLYYYETDYDTSRNIRENLYVKID | 147 | |
| DB | 85 | NWVPNSAKRIYVELKFTLRDCNSIPVLGTGCKETFNLYYVESDDHGVKPREHQFTIID | 144 | |
| QY | 148 | TIADDESTQGLDERKKKLTNTEVREIGPLSKSGFYLAFOVGCALVSVKYYKKCMT | 207 | |
| DB | 145 | TIADDESTQGLDRLIKLTETREVGPPVKKGFYLAFOVGACVALVSVRYVFKKPF | 204 | |
| QY | 208 | IVENLAVEPDVTGSEFSLVEVAGTCVSAEEAEANSPRMCSAEGEMLVPIGCKICA | 267 | |
| DB | 205 | TVKNLAMPDPDTPV--MDSQSLVEVAGSCVNNKSKE--EDPRMYCSTGEMLVPIGCKSCNA | 261 | |
| QY | 268 | GYQCKGDTCECGCKRPFYKSSSQDIDQSCRCPLHNSFDREGSSRCCEQDYVAPSDPPVA | 327 | |
| DB | 262 | GYERGFQCAQCRPGFYALDGNKKCAKCPHSSSTQEDGSMNCCENNYFPADKDPBMA | 321 | |
| QY | 328 | CTRPSPAPQNLFININQTTVSLSEMSPRADNGRDVTRILCKKCSWEOGECVPCSGNISG | 387 | |
| DB | 322 | CTRPSPSRNVIKSNINETSVLDMSPWLDIGRQDVFNIIICKCGMMIHKCEPCSPVVR | 381 | |
| QY | 388 | YMPQQTGLEDNYVTVMDLAAHANTTFEVEAVNGVSDSRQRLPRAVSIITGQAAPSOVS | 447 | |
| DB | 382 | FLPQFGTLNTVTVTDLIAHTNTVFELDANVGSELSPPROFAAVSIITNOAPSPVL | 441 | |
| QY | 448 | GWMEKRVLOREVOCLSMOEPHPNVITFYEELKYEKOOREBTGYLTKTSTASINLKP | 507 | |
| DB | 442 | TIKKDRISRNSISLSWQEPHPNGIILDYKATYKQOEQESYITLIRKGTNVTISSLKP | 501 | |
| QY | 508 | GTVVVFOIRATTAAGYGNVSPRLVATLLEBASGKFEATPAVSEONPYIIIAVVAVACTI | 567 | |
| DB | 502 | DTIVVFOIRATTAAGYGTNSRKKPEPESP-----DFSISGSSQVVMIAISAVALI | 554 | |
| QY | 568 | ILVEMVFGFIIIGRRHCGYSKADQEGDEDELYHSLVTNHELSV | 609 | |
| DB | 555 | ILTVIIV--VLIG-RFCGYSKHGADKKLHF-----GNGHKL | 590 | |

Search completed: August 23, 2005, 08:30:04
Job time : 73.5744 secs

DR SMART; SM00220; S TKC; 1.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 23, 2005, 08:30:14 ; Search time 109.563 Seconds

(without alignments)
2180.182 Million cell updates/sec

Title: US-10-073-064-3
Perfect score: 3243
Sequence: 1 MVQTRPSPWILLCYWLLG.....EGDELYFSLVTEHLSVL 610

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1759131 seqs, 391586102 residues

Total number of hits satisfying chosen parameters: 1759131

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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2: /cgn2_6/prodata/2/pubppaa/PCT_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Length | ID | Description |
|------------|--------|--------------|----------------------------|--------------------|
| 1 | 3191 | 98.4 | 998 10 US-09-823-187-42 | Sequence 42, App1 |
| 2 | 3175 | 97.9 | 998 10 US-09-823-187-43 | Sequence 43, App1 |
| 3 | 3139 | 96.8 | 945 15 US-10-112-944-260 | Sequence 260, App1 |
| 4 | 3139 | 96.8 | 998 10 US-09-823-187-40 | Sequence 40, App1 |
| 5 | 3031.5 | 93.5 | 993 10 US-09-823-187-39 | Sequence 39, App1 |
| 6 | 3031.5 | 93.5 | 993 10 US-09-823-187-41 | Sequence 41, App1 |
| 7 | 1843 | 56.8 | 991 10 US-09-823-187-44 | Sequence 44, App1 |
| 8 | 1838.5 | 56.7 | 1041 18 US-10-840-512-215 | Sequence 215, App1 |
| 9 | 1832.5 | 56.4 | 953 14 US-10-412-277-7 | Sequence 7, App1 |
| 10 | 1829 | 56.2 | 991 17 US-10-732-923-13667 | Sequence 13667, A |
| 11 | 1821 | 56.2 | 1005 15 US-10-029-020-63 | Sequence 63, App1 |

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| 12 | 1819 | 56.1 | 1037 14 US-10-316-124-3 | Sequence 3, App1 |
| 13 | 1819 | 56.1 | 1037 15 US-10-353-690-40 | Sequence 40, App1 |
| 14 | 1819 | 56.1 | 1037 20 US-11-064-551-3 | Sequence 3, App1 |
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| 16 | 1802 | 55.6 | 1013 17 US-10-732-923-13668 | Sequence 13668, A |
| 17 | 1799 | 55.5 | 666 9 US-09-771-161A-136 | Sequence 136, App |
| 18 | 1799 | 55.5 | 983 9 US-09-771-161A-227 | Sequence 227, App |
| 19 | 1799 | 55.5 | 983 14 US-10-205-823-97 | Sequence 97, App1 |
| 20 | 1799 | 55.5 | 983 14 US-10-345-680-2 | Sequence 2, App1 |
| 21 | 1799 | 55.5 | 983 15 US-10-295-027-602 | Sequence 602, App |
| 22 | 1799 | 55.5 | 983 15 US-10-029-020-59 | Sequence 59, App1 |
| 23 | 1799 | 55.5 | 983 17 US-10-794-514A-467 | Sequence 467, App |
| 24 | 1799 | 55.5 | 983 18 US-10-489-125B-11 | Sequence 11, App1 |
| 25 | 1788.5 | 55.1 | 985 15 US-10-029-020-61 | Sequence 61, App1 |
| 26 | 1786.5 | 55.1 | 968 14 US-10-412-277-6 | Sequence 6, App1 |
| 27 | 1786.5 | 55.1 | 983 17 US-10-732-923-13675 | Sequence 13675, A |
| 28 | 1736.5 | 53.5 | 921 9 US-09-805-020-52 | Sequence 52, App1 |
| 29 | 1736.5 | 53.5 | 986 16 US-10-723-860-597 | Sequence 597, App |
| 30 | 1729.5 | 52.3 | 1104 9 US-09-982-610-36 | Sequence 36, App1 |
| 31 | 1701.5 | 52.5 | 935 15 US-10-449-569-36 | Sequence 36, App1 |
| 32 | 1701.5 | 52.5 | 992 10 US-09-973-424A-53 | Sequence 53, App1 |
| 33 | 1701.5 | 52.5 | 992 10 US-09-973-424A-53 | Sequence 53, App1 |
| 34 | 1701.5 | 52.5 | 992 17 US-10-691-165-5 | Sequence 5, App1 |
| 35 | 1701.5 | 52.5 | 992 17 US-10-691-165-53 | Sequence 53, App1 |
| 36 | 1701.5 | 52.5 | 1005 15 US-10-449-569-2 | Sequence 2, App1 |
| 37 | 1701.5 | 52.5 | 1012 15 US-10-168-582-3 | Sequence 3, App1 |
| 38 | 1699.5 | 52.4 | 935 15 US-10-449-569-34 | Sequence 34, App1 |
| 39 | 1695 | 52.3 | 991 10 US-09-973-424A-52 | Sequence 52, App1 |
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| 41 | 1676 | 51.7 | 1035 15 US-10-029-020-20 | Sequence 20, App1 |
| 42 | 1670.5 | 51.5 | 1036 14 US-09-971-708-2 | Sequence 2, App1 |
| 43 | 1670.5 | 51.5 | 1036 14 US-10-245-752-104 | Sequence 104, App |
| 44 | 1670.5 | 51.5 | 1036 14 US-10-245-859-104 | Sequence 104, App |
| 45 | 1670.5 | 51.5 | 1036 14 US-10-245-103-104 | Sequence 104, App |

ALIGNMENTS

RESULT 1
US-09-823-187-42
: Sequence 42, Application US/09823187
: Publication No. US20030096952A1
GENERAL INFORMATION:
APPLICANT: Burgess, Catherine
APPLICANT: Gusev, Vladimir Y
APPLICANT: Liu, Xiaohong
APPLICANT: Majumder, Kund
APPLICANT: Padigaru, Muralidhar
APPLICANT: Patnrajan, Meera
APPLICANT: Shinkets, Richard A
APPLICANT: Spaderna, Steven K
APPLICANT: Spytek, Kimberly
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-745
CURRENT APPLICATION NUMBER: US/09/823, 187
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: 60/193,339
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/193,205
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/195,343
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: 60/195,088
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,005
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,792
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: 60/196,556
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 60/197,081

; PRIOR FILING DATE: 2000-04-13
 ; PRIOR APPLICATION NUMBER: 60/197,525
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/197,087
 ; PRIOR FILING DATE: 2000-04-14
 ; NUMBER OF SEQ ID NOS: 103
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 42
 ; LENGTH: 998
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-823-187-42

Query Match 98.4%; Score 3191; DB 10; Length 998;
 Best Local Similarity 100.0%; Pred. No. 6,7e-244;
 Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 541 KMFATVVSSEONPVIIIAVAVAGTIIIVMVFGLIGRRHCGYSKADCEGDEBELYFH 599

RESULT 2

; Sequence 43, Application US/09823187
 ; Publication No. US20030096952A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Burgess, Catherine
 ; APPLICANT: Gusev, Vladimir Y
 ; APPLICANT: Liu, Xiaohong
 ; APPLICANT: Majumder, Kumud
 ; APPLICANT: Padigaru, Muralidhar
 ; APPLICANT: Paturajan, Meera
 ; APPLICANT: Shimkeas, Richard A
 ; APPLICANT: Spaderna, Steven K
 ; APPLICANT: Spytek, Kimberly
 ; APPLICANT: Taupier, Raymond J

; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
 ; FILE REFERENCE: 15966-745
 ; CURRENT APPLICATION NUMBER: US/09/823,187
 ; CURRENT FILING DATE: 2001-03-29
 ; PRIOR APPLICATION NUMBER: 60/193,339
 ; PRIOR FILING DATE: 2000-03-30
 ; PRIOR APPLICATION NUMBER: 60/193,205
 ; PRIOR FILING DATE: 2000-03-30
 ; PRIOR APPLICATION NUMBER: 60/195,343
 ; PRIOR FILING DATE: 2000-04-05
 ; PRIOR APPLICATION NUMBER: 60/195,088
 ; PRIOR FILING DATE: 2000-04-06
 ; PRIOR APPLICATION NUMBER: 60/195,005
 ; PRIOR FILING DATE: 2000-04-06
 ; PRIOR APPLICATION NUMBER: 60/195,792
 ; PRIOR FILING DATE: 2000-04-10
 ; PRIOR APPLICATION NUMBER: 60/196,556
 ; PRIOR FILING DATE: 2000-04-11
 ; PRIOR APPLICATION NUMBER: 60/197,081
 ; PRIOR FILING DATE: 2000-04-13
 ; PRIOR APPLICATION NUMBER: 60/197,525
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/197,087
 ; NUMBER OF SEQ ID NOS: 103
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 43
 ; LENGTH: 998
 ; TYPE: PRT
 ; ORGANISM: Rattus norvegicus
 US-09-823-187-43

Query Match 97.2%; Score 3175; DB 10; Length 998;
 Best Local Similarity 99.2%; Pred. No. 1.2e-242;
 Matches 594; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 MVTOTRPPSWIILCYIMLGFHAGTGAQAQAVLLDSKAQOQTELEWISSPPSGWBEISG 60
 DB 1 MVTOTRPPSWIILCYIMLGFHAGTGAQAQAVLLDSKAQOQTELEWISSPPSGWBEISG 60
 QY 61 LDENVYPIRTYQVQVWEPNQNMLRTNMTSKGNAORIFVELKFTLRDCKSLPGVLTCK 120
 DB 61 LDENVYPIRTYQVQVWEPNQNMLRTNMTSKGNAORIFVELKFTLRDCKSLPGVLTCK 120
 QY 121 ETFNLYYETDYGTRNIRENLVYKIDTIADESFTQDGERKMKLNTVEIREIGPLSKK 180
 DB 121 ETFNLYYETDYGTRNIRENLVYKIDTIADESFTQDGERKMKLNTVEIREIGPLSKK 180
 QY 181 GFYLAPODVACIALVSVKYYKKCWTIVENLAVFPDYTGSEFSSLVEVRGTCVSSAE 240
 DB 181 GFYLAPODVACIALVSVKYYKKCWTIVENLAVFPDYTGSEFSSLVEVRGTCVSSAE 240
 QY 241 EAENSPRMHCSAAGEMLVPIGKICAKGYOQKGDTCPCGRFRYKSSSOLQCSRCPETHS 300
 DB 241 EAENSPRMHCSAAGEMLVPIGKICAKGYOQKGDTCPCGRFRYKSSSOLQCSRCPETHS 300
 QY 301 FSDREGSSRCECEDGYRAPSDPPYVACTRPSPAPNLIFFINQTTVLSLEWSPADNGGR 360
 DB 301 FSDREGSSRCECEDGYRAPSDPPYVACTRPSPAPNLIFFINQTTVLSLEWSPADNGGR 360
 QY 361 NDVTYRILCKRCSEWQECVPCGSNIGMPQOTGLENDNYTVMDLAHANYTFEEVAVNG 420
 DB 361 NDVTYRILCKRCSEWQECVPCGSNIGMPQOTGLENDNYTVMDLAHANYTFEEVAVNG 420
 QY 421 VSDLSRSQRLFAAVSITTTGAAPSOVSGWKEKERVLSVOLSWQEPHHPGVITTEYIKY 480
 DB 421 VSDLSRSQRLFAAVSITTTGAAPSOVSGWKEKERVLSVOLSWQEPHHPGVITTEYIKY 480
 QY 481 YEKDQERTYSTLTKTSTASINNLKPGTVYVFOIRAVTAAGYGNYSPLDVAATLEASG 540
 DB 481 YEKDQERTYSTLTKTSTASINNLKPGTVYVFOIRAVTAAGYGNYSPLDVAATLEASG 540
 QY 541 KMFATVVSSEONPVIIIAVAVAGTIIIVMVFGLIGRRHCGYSKADCEGDEBELYFH 599

Db 541 KMFEATAVSSSEQNPVITIIAIVAVAGTIIIVFMVGFIIIGRRHCGYSKADQGDDELYFH 599

RESULT 3

US-10-112-944-260
Sequence 260, Application US/10112944
Publication No. US20040048249A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Yang, Yonghong
APPLICANT: Zheng, Gezhi
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Xue, Aidong J.
APPLICANT: Wang, Jian-Rui
APPLICANT: Wehrman, Tom
APPLICANT: Ghosh, Malabika
APPLICANT: Wang, Dunrui
APPLICANT: Zhao, Qing A.
APPLICANT: Wang, Zhiwei
TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
TITLE OF INVENTION: Secreted Polypeptides
FILE REFERENCE: 805A
CURRENT FILING DATE: US/10/112,944
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000/01-25
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/515,126
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: US 09/519,705
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 09/552,929
PRIOR FILING DATE: 2000-04-18
PRIOR APPLICATION NUMBER: US 09/577,408
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 924
SOFTWARE: PL_Fl_genes Version 5.0
SEQ ID NO 260
LENGTH: 945
TYPE: PRT
ORGANISM: Homo sapiens
US-10-112-944-260

Query Match 96.8%; Score 3139; DB 15; Length 945;

Best Local Similarity 97.7%; Pred. No. 8.3e-240; Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

QY 1 MVTOTRPSWIIICITWILGFAHTGEAQAEBVLILDSKAQOTLEWISSPPSGWEISG 60
DB 1 MVTOTRPSWIIICITWILGFAHTGEAQAEBVLILDSKAQOTLEWISSPPSGWEISG 60
QY 61 LDENVTPRTYOVQCVMEPNONNLRTWISKNAQRIFVELKFTLRDQNSLPVYLGTCK 120
DB 61 LDENVTPRTYOVQCVMEPNONNLRTWISKNAQRIFVELKFTLRDQNSLPVYLGTCK 120
QY 121 ETFNLVYETDYGGRNIRENLVYKIDITIADESFTQDLSERKMKLNTVEIREIGPLSKK 180
DB 121 ETFNLVYETDYGGRNIRENLVYKIDITIADESFTQDLSERKMKLNTVEIREIGPLSKK 180
QY 181 GFYLAFOVGACIALVSVKYYKKCWITIVENLAVFPDVTGSEFSLVEVAGTCVSSAAE 240
DB 181 GFYLAFOVGACIALVSVKYYKKCWITIVENLAVFPDVTGSEFSLVEVAGTCVSSAAE 240
QY 241 EAENSPPRHGASGEHMLVPIGKCTICKAGYQOKGDTCEPCGRFPYKSSQDLQCSRCPHHS 300
DB 241 EAENAPRHGASGEHMLVPIGKCTICKAGYQOKGDTCEPCGRFPYKSSQDLQCSRCPHHS 300

QY 301 FSDREGSSRCECEDGYRAESDPPIYVACTRPPSAPQNLIFINQTVLSLEMSPPADNGCR 360
DB 301 FSDREGSSRCECEDGYRAESDPPIYVACTRPPSAPQNLIFINQTVLSLEMSPPADNGCR 360
QY 361 NDVTYRILCKRSGMEQCEVPCGSGNIGMPQOTGLEDNYVTVMULLAHANTFEVEAVNG 420
DB 361 NDVTYRILCKRSGMEQCEVPCGSGNIGMPQOTGLEDNYVTVMULLAHANTFEVEAVNG 420
QY 421 VSDLSRSQRLFAAVSITTGQAAPQVSGWKERVLDSVLSWQEPHPNVTIYEYIKY 480
DB 421 VSDLSRSQRLFAAVSITTGQAAPQVSGWKERVLDSVLSWQEPHPNVTIYEYIKY 480
QY 481 YEKDQERTYSTLTKKSTASINNLKPGTYVYQIRAVTAAGYGNYSFRLDVATLEASG 540
DB 481 YEKDQERTYSTVTKSTASINNLKPGTYVYQIRAVTAAGYGNYSFRLDVATLEASG 540
QY 541 KMFEATAVSSSEQNPVITIIAIVAVAGTIIIVFMVGFIIIGRRHCGYSKADQGDDELYFH 599
DB 541 KMFEATAVSSSEQNPVITIIAIVAVAGTIIIVFMVGFIIIGRRHCGYSKADQGDDELYFH 599

RESULT 4

US-09-823-187-40
Sequence 40, Application US/09823187
Publication No. US20030096952A1
GENERAL INFORMATION:
APPLICANT: Burgess, Catherine
APPLICANT: Gusev, Vladimir Y
APPLICANT: Liu, Xiaohong
APPLICANT: Majumder, Kumud
APPLICANT: Padigar, Muralidhar
APPLICANT: Patturajan, Meera
APPLICANT: Shinkets, Richard A
APPLICANT: Spaderna, Steven K
APPLICANT: Spytek, Kimberly
APPLICANT: Taupier, Raymond J
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-745
CURRENT APPLICATION NUMBER: US/09/823,187
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/193,339
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/193,205
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/195,343
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: 60/195,088
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,005
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,792
PRIOR FILING DATE: 2000-04-10
PRIOR APPLICATION NUMBER: 60/196,556
PRIOR FILING DATE: 2000-04-11
PRIOR APPLICATION NUMBER: 60/197,081
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 60/197,525
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/197,087
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 103
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 40
LENGTH: 998
TYPE: PRT
ORGANISM: Homo sapiens
US-09-823-187-40

Query Match 96.8%; Score 3139; DB 10; Length 998;

Best Local Similarity 97.7%; Pred. No. 9e-240; Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0;


```

QY 1 MVTQTRPSPWIIICYLWLGFAHTGEAQAKEYLLDLSKAQOTELEMISSPPSGMEISG 60
DB 1 MVEQTRPSWIIICYLWLGFAHTGEAQAKEYLLDLSKAQOTELEMISSPPSGMEISG 60
QY 61 LDENYTPIRTYQVCQWEPNOMNMLRTNWSKGAQRIFVELKFTLRDCNSLPVIGTCK 120
DB 61 LDENYTPIRTYQVCQWEPNOMNMLRTNWSKGAQRIFVELKFTLRDCNSLPVIGTCK 120
QY 121 ETEFLYYETDVTGGRNIRENLVYKIDTIAADESFTQGLGERMKLNTREIIGPLSKK 180
DB 121 ETEFLYYETDVTGGRNIRENLVYKIDTIAADESFTQGLGERMKLNTREIIGPLSKK 180
QY 181 GFYLAFOVDGACIALVSVKYYKKCWTIVENLAVPDTVTGSESSLVEVRGTCVSSAEE 240
DB 181 GFYLAFOVDGACIALVSVKYYKKCWTIVENLAVPDTVTGSESSLVEVRGTCVSSAEE 240
QY 241 EAENSPRMHCSABGEMLVPIGKICCKAGYQOKGDTCEPCGGRFYKSSSDILQSCRCPHTS 300
DB 241 EAENSPRMHCSABGEMLVPIGKICCKAGYQOKGDTCEPCGGRFYKSSSDILQSCRCPHTS 300
QY 301 FSDREGSSRCECEDGYRAPSDEPPYVACTRPPSAPQNLIFINQTTVSLSESPPADNGGR 360
DB 301 FSDREGSSRCECEDGYRAPSDEPPYVACTRPPSAPQNLIFINQTTVSLSESPPADNGGR 360
QY 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQOTGLEBDNYVTVDLLAHANYTREVAVNG 420
DB 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQOTGLEBDNYVTVDLLAHANYTREVAVNG 420
QY 421 VSDLSRSQRLFAAVSITTTGQAAPSOVSQWKEKRLQRSVQLSWQEBEHPNGVITEYEIKY 480
DB 421 VSDLSRSQRLFAAVSITTTGQAAPSOVSQWKEKRLQRSVQLSWQEBEHPNGVITEYEIKY 480
QY 481 YEKDQERERTYSTLTKSTASINNLKPGTYVYFQIRAVTAAGYGNVSPRLDVATLEBASG 540
DB 481 YEKDQERERTYSTLTKSTASINNLKPGTYVYFQIRAVTAAGYGNVSPRLDVATLEBASG 540
QY 541 KMEFATVSSSEQNPVITIAVAVAGTIIIVFMVFGIIGRRHCGYSKADQEGDELYFH 599
DB 541 KMEFATVSSSEQNPVITIAVAVAGTIIIVFMVFGIIGRRHCGYSKADQEGDELYFH 599

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RESULT 5
US-09-823-187-39
; Sequence 39, Application US/09823187
; Publication No. US20030096952A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine
; APPLICANT: Liu, Xiaohong
; APPLICANT: Majumder, Kumud
; APPLICANT: Padigaru, Muralidhar
; APPLICANT: Patnrajan, Meera
; APPLICANT: Shimketa, Richard A
; APPLICANT: Spaderna, Steven K
; APPLICANT: Szytek, Kimberly
; APPLICANT: Taupier, Raymond J
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-745
; CURRENT APPLICATION NUMBER: US/09/823,187
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/193,339
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/193,205
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 60/195,343
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/195,088
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,005
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,792
; PRIOR FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: 60/196,556

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; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: 60/197,081
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/197,525
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/197,087
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 993
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-823-187-39
Query Match          93.5%; Score 3031.5; DB 10; Length 993;
Best Local Similarity 94.5%; Pred. No. 3e-231;
Matches 566; Conservative 17; Mismatches 11; Indels 5; Gaps 1;
QY 1 MVTQTRPSPWIIICYLWLGFAHTGEAQAKEYLLDLSKAQOTELEMISSPPSGMEISG 60
DB 1 MVTQTRPSPWIIICYLWLGFAHTGEAQAKEYLLDLSKAQOTELEMISSPPSGMEISG 60
QY 61 LDENYTPIRTYQVCQWEPNOMNMLRTNWSKGAQRIFVELKFTLRDCNSLPVIGTCK 120
DB 61 LDENYTPIRTYQVCQWEPNOMNMLRTNWSKGAQRIFVELKFTLRDCNSLPVIGTCK 120
QY 121 ETEFLYYETDVTGGRNIRENLVYKIDTIAADESFTQGLGERMKLNTREIIGPLSKK 180
DB 121 ETEFLYYETDVTGGRNIRENLVYKIDTIAADESFTQGLGERMKLNTREIIGPLSKK 180
QY 181 GFYLAFOVDGACIALVSVKYYKKCWTIVENLAVPDTVTGSESSLVEVRGTCVSSAEE 240
DB 181 GFYLAFOVDGACIALVSVKYYKKCWTIVENLAVPDTVTGSESSLVEVRGTCVSSAEE 240
QY 241 EAENSPRMHCSABGEMLVPIGKICCKAGYQOKGDTCEPCGGRFYKSSSDILQSCRCPHTS 300
DB 241 EAENSPRMHCSABGEMLVPIGKICCKAGYQOKGDTCEPCGGRFYKSSSDILQSCRCPHTS 300
QY 301 FSDREGSSRCECEDGYRAPSDEPPYVACTRPPSAPQNLIFINQTTVSLSESPPADNGGR 360
DB 301 FSDREGSSRCECEDGYRAPSDEPPYVACTRPPSAPQNLIFINQTTVSLSESPPADNGGR 360
QY 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQOTGLEBDNYVTVDLLAHANYTREVAVNG 420
DB 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQOTGLEBDNYVTVDLLAHANYTREVAVNG 420
QY 421 VSDLSRSQRLFAAVSITTTGQAAPSOVSQWKEKRLQRSVQLSWQEBEHPNGVITEYEIKY 480
DB 421 VSDLSRSQRLFAAVSITTTGQAAPSOVSQWKEKRLQRSVQLSWQEBEHPNGVITEYEIKY 480
QY 481 YEKDQERERTYSTLTKSTASINNLKPGTYVYFQIRAVTAAGYGNVSPRLDVATLEBASG 540
DB 481 YEKDQERERTYSTLTKSTASINNLKPGTYVYFQIRAVTAAGYGNVSPRLDVATLEBASG 540
QY 541 KMEFATVSSSEQNPVITIAVAVAGTIIIVFMVFGIIGRRHCGYSKADQEGDELYFH 599
DB 541 KMEFATVSSSEQNPVITIAVAVAGTIIIVFMVFGIIGRRHCGYSKADQEGDELYFH 599

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RESULT 6
US-09-823-187-41
; Sequence 41, Application US/09823187
; Publication No. US20030096952A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine
; APPLICANT: Liu, Xiaohong
; APPLICANT: Majumder, Kumud
; APPLICANT: Patnrajan, Meera
; APPLICANT: Shimketa, Richard A
; APPLICANT: Spaderna, Steven K

```

| Query Match | 93.5% | Score 3031.5 | DB 10 | Length 993 |
|-----------------------|-------|---|---------------|------------|
| Best Local Similarity | 94.5% | Pred. No. 3e-221 | | |
| Matches | 566 | Conservative 17 | Mismatches 11 | Indels 5 |
| | | | | Gaps 1 |
| QY | 1 | MVVOITRPSMIILCYIMLGFATHTGEAQAKEVLLDLSKAQOTELEWISSPSPGMBEISG | 60 | |
| DB | 1 | MLHRSRLPEPMTLCSVMLRFAHGTGEAQAKEVILLDSKAQOTELEWISSPPNGMBEISG | 60 | |
| QY | 61 | LDENYTPTRITYOVCCWMEPNONNMLRTWISKNAQRIFVBLKFTLRDONSIPGLVLTCK | 120 | |
| DB | 61 | LDENYTPTRITYOVCCWMEPNONNMLRTWIKAKSNQRIFVEIKFTLRDONSIPGLVLTCK | 120 | |
| QY | 121 | ETFLYYEENDYDGRNIRENLYVKIDITIADESEFTQDILGRKKMLTEVREIGPLSKK | 180 | |
| DB | 121 | ETFLYYEETDYDGRNIRENOYKIDITIADESEFTQDILGRKKMLTEVREIGPLSKK | 180 | |
| QY | 181 | GFYLAFOADVACIALVSVKYYKKCMTITVENLAVPDPVTGSEFSLSLVEBGTCVASAEE | 240 | |
| DB | 181 | GFYLAFOADVACIALVSVKYYKKCMTIIEMLAIFPDVITGSEBSLSLVEBGTCVASAEE | 240 | |
| QY | 241 | EAENSPRMHGSABEGEWLVPICKCTICKAGYQOKDTCBPCGRRFYKSSQDILQCSRPTHS | 300 | |
| DB | 241 | EAENSPKMHGCAEGEWLVPICKCTICKAQQOKDTCBPCGCGFYKSSQDILQCSRPTHS | 300 | |
| QY | 301 | PSDEGSRCECEGCVYRAPSPDPVYACTRPPSAQONLIENINQTTVLEMSPPADNGR | 360 | |
| DB | 301 | PSDEGSRCECEGCVYRAPSPDPVYACTRPPSAQONLIENINQTTVLEMSPPADNGR | 360 | |
| QY | 361 | NDVYTRILCKKCSMEQECVPCGSNIGVMPQOTGLJEDNYVYVMDLTAANTFVEAANG | 420 | |
| DB | 361 | NDVYTRILCKKCSMEQECVPCGSNIGVMPQOTGLVDNYVYVMDLTAANTFVEAANG | 420 | |
| QY | 421 | VSDLSRSQRLFAVASITTTGAAPSPGVSGVMKERVLORSVOLUSQSPDEHPNGVITEIKY | 480 | |
| DB | 421 | VSDLSRSQRLFAAVASITTTGAAPSPGVSGVMKERVLORSVELUSQSPDEHPNGVITEIKY | 480 | |
| QY | 481 | YEKQORETYSFTLKTKTSASINNLKPGTVYVFOJRAATAGYGYNSRDLVATLEBSG | 540 | |
| DB | 481 | YEKQORETYSFTVTKRSTASINNLKPGTVYVFOJRAATAGYGYNSRDLVATLEBSG | 539 | |

Qy 6 RPSW--IILCYIWMILGFARHGEAOAAEYVLLIBSKAQOTLEWISSPSCMEIISGLDE 63
Db 13 RABLMTCLLC-----AALRTLLASPSNEVLLIBSRITWGMGLMIAPKNGMEIGEYDE 67
Qy 64 NYPIRTYOVCOVMEBPNQNNMLRTWMSKGAORIFVELKFTLDCNSLPGLVGTCKETP 123
Db 68 NYAPIHTYOVCKYMBQNNQNNMLTWSINEGASRIFFELKFTLDCNSLPGLVGTCKETP 127
Qy 124 NLYYIETDYDTGNIRRENL.YKIDITLADDESTQDGLERKMKANTEVREI::GLSKSGFY 183
Db 128 NMYYFESDQONRNRIKENOYIKIDITLADDESTFELDLDRVWKNTREVRDVGPSLKKGFY 187
Qy 184 LARQVDGACIALVSVKVVKKYKCMFTVENLAVFPPIVVGSEFSSLVEVRGTGVSAEAEAL 243
Db 188 LARQVDGACIALVSVKVVKKYKCPVVRHRAVFPDITITGDSQLLEVSGSCCN--HSVTD 245

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Qy 244 NSPRMCSAEGEMLVPIGKCI CKAQYQOKGDTCEPCGRFRYKSSSDLOCS RCPTHSFSD 303
Db 246 EPPMHCASAGEMLVPIGKCMCKAGYEKNGTCQVCPGPFKASPHIQSCGKCPHXYTH 305
Qy 304 REGSSRECECDGYRAPSDPPYVACTRPPAPQULININQTYSLFMSPPANNGENDV 363
Db 306 EELSTSCVCEKDYFRRESDDPTWACTRPPAPRAISNVNSETSYFLWIPADGGKDV 365
Qy 364 TYRILCRCSWEGECVPCGSNIGMPQGTGLDENVYTVMDLLAHANYTEEVEAVNGVD 423
Db 366 SYYLACKCKSHAGVCECGHVRYLPRQGLKNTSYVMWMDLAHTYTFEIEAVNGVSD 425
Qy 424 LSRNQRLFAVSTTGGAPSDQVSGWKEKRVLRQSVOLSNQEPHNGVITTEIKYEEK 483
Db 426 LSPBARQVSVNVTNNQAPSDPTNVKKGKIAKNSISLSWQEPDRPNCIILLEYEIKHEK 485
Qy 484 DQERTYSLTKTSTASINNLKRGTYVYFOIRAVTAAGVNSPRLDVATLEBASGMF 543
Db 486 DQ-ETSTYTIKSKETITLTAAGLKPAASYVFOIRAKRTAGVGSRRPE-----F 533
Qy 544 EAT---AVSEQNPIIIIAVAVAGTIIIVFVFGFIIGRHGCGSKADQGDDE-LYFH 539
Db 534 ETPPVFASSDQSQIPPIAVSVTWG-VILLAVIGVLLSGRCGYSKAKQLEPEEKHFH 592
Qy 600 SLVTNEHLAV 609
Db 593 ----NGHIKL 598
```

```
RESULT 8
US-10-840-512-215
; Sequence 215, Application US/10840512
; Publication No. US20050125852A1
; GENERAL INFORMATION:
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: MANNING, GERRARD
; APPLICANT: CHARIDCZAK, GLEN
; APPLICANT: GRIGORIEV, IGOR
; TITLE OF INVENTION: NOVEL KINASES
; FILE REFERENCE: 034536-1455
; CURRENT APPLICATION NUMBER: US/10/840, 512
; CURRENT FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: 60/469, 014
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 239
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 215
; LENGTH: 1041
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-840-512-215
```

```
Query Match 56.7%; Score 1838.5; DB 18; Length 1041;
Best Local Similarity 54.8%; Pred. No. 1.5e-136;
Matches 352; Conservative 98; Mismatches 135; Indels 57; Gaps 11;

Qy 6 RPSMWILCY-----IW-----LLGFAHTGEAQAQAEVLLLDLSKAQOTLEWISSPPSG 54
Db 25 RVAPSLAGCYSAPLKGMLWCLLICALRTLILASPSNEVNLDSRTWGLGWIAPFKNG 84
Qy 55 WEETSGLDENYTPRTTYQVCQWNEPNONNMLRTNWSKNAQRI FVELKTLTADCNLPG 114
Db 85 WEETGEDEVENYAPHTTYQVCKMEONONNMLTSMINEGASRI FIELKFTLADCNLPG 144
Qy 115 VILGCKETPLUYVETDYDGRNIRENLVYKIDITLADSFQSGDGERMGLNTEVREI 164
Db 145 GLIGCKETPLNMYTFESDDENGRSIKENQYIKIDITLADSFTELDLDRWKLNTEVRDV 204
Qy 175 GPLSKGFFYLAFOVAGACIALVSKVYVKKCWITVENILAVFPDVTGSESSILEVYAGTC 234
Db 205 GPLSKGFFYLAFOVAGACIALVSKVYVKKCPSVYRLALFPDITLADSEQLLEVSGSC 264
Qy 235 VSSAEEBAENSPRMHCASBEGMLVPIGKCI CKAQYQOKGDTCEPCGRFRYKSSSDLOCS 294
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Db 265 VN--HSVTDDPPMHCASAGEMLVPIGKCMCKAGYEKNGTCQVCPGPFKASPHSQOTS 322
Qy 295 RCPTHSFSDREGSSRECECDGYRAPSDPPYVACTRPPAPQULININQTYSLFMSPP 354
Db 323 KCPPHSYTHEASTSCVCEKDYFRKSDPTWACTRPPAPRAISNVNSETSYFLWIP 382
Qy 355 ADNGRNDVYTYRILCRCSWEGECVPCGSNIGMPQGTGLDENVYTVMDLLAHANYTEE 414
Db 383 ADTGKRDVSYTYLACKCKNSHAGVCECGHVRYLPRQGLKNTSYVMWMDLAHTYTFE 442
Qy 415 VEAVNGVSDLSRQRLFAVSTTGGAPSDQVSGWKEKRVLRQSVOLSNQEPHNGVIT 474
Db 443 IEAVNGVSDLSPTGRQVSVNVTNNQAPSDPTNVKKGKIAKNSISLSWQEPDRPNCIIL 502
Qy 475 EYEIKYEEKDQERTYSLTKTSTASINNLKRGTYVYFOIRAVTAAGVNSPRLDVAT 534
Db 503 EYEIKYEEKDQ-ETSTYTIKSKETITLTAAGLKPAASYVFOIRAKRTAGVGSRRPE--- 558
Qy 535 LEBASGMFEAT---AVSEQNPIIIIAVAVAGTIIIVFVFGFI-----GRR 581
Db 559 -----FETTVSVASANDQSQIPPIAVSVTWG-VILLAVI-LGPLSGSCCDDCCGRA 609
Qy 582 -----HCGYSKADQGDDE-LYFHSLVNNEHLAV 609
Db 610 SSLCAVAHPBSLIWRGCGYSKAKQDPEEEKHFH----NGHIKL 647
```

```
RESULT 9
US-10-412-277-7
; Sequence 7, Application US/10412277
; Publication No. US20030175791A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001067DIV
; CURRENT APPLICATION NUMBER: US/10/412, 277
; CURRENT FILING DATE: 2003-04-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 953
; TYPE: PRT
; ORGANISM: Human
US-10-412-277-7
```

```
Query Match 56.5%; Score 1832.5; DB 14; Length 953;
Best Local Similarity 58.2%; Pred. No. 4e-136;
Matches 340; Conservative 96; Mismatches 125; Indels 23; Gaps 7;

Qy 30 AKEVLLDLSKAQOTLEWISSPPSGWEETSGLDENYTPRTTYQVCQWNEPNONNMLRTNM 89
Db 1 SNEVNLDSRTTWGDLGWIAPFKNGWEETSGDEVENYAPHTTYQVCKMEONONNMLTSM 60
Qy 90 ISKNAQRIFVELKFTLRDNCNSLPGLGTCCKETPLNYYETDYDGRNIRENLVYKIDIT 149
Db 61 ISNEGASRI FIELKFTLRDNCNSLPGLGTCCKETPLNYYETDYDGRNIRENLVYKIDIT 120
Qy 150 AADESTQGLDERKKKLNTVEIREIPLSKKGYLAFOVAGACIALVSKVYVKKCWITV 209
Db 121 AADESTTELDIGRWVKNLNTVEADVPLSKKGYLAFOVAGACIALVSKVYVKKCPSSV 180
Qy 210 ENLAVPDPVITGSEPSLVNVRGTQVSSAEEBAENSPRMHCASBEGMLVPIGKCI CKAQY 269
Db 181 RHLAVPDPVITGSDSGLLEVSQVYN--HSVTDEPPMHCASBEGMLVPIGKCMCKAGY 238
Qy 270 QQKGDTCPCPGRRFRYKSSSDLOCSRCPTHSFSDREGSSRECECDGYRAPSDPPVYACT 329
Db 239 EEKNGTCQVCRPBFQASPHIQSCGKCPHASTHEASTSCVCEKDYFRRESDPFPMAC 258
Qy 330 RPPAPQULININQTYSLFMSPPANNGRNDVYTYRILCRCSWEGECVPCGSNIGTYM 389
```

```
Db 299 RPPAPRAVAISNVNMTSVLEMIIPADTQGRKDVSYIACKKCNHAGVCECGHVRYL 358
Qy 390 PQOQLENTYTMWDLAHANTYFEVENVNVSLSRQRLPAVASITTGQAASQVSGV 449
Db 359 PROGLKNTSVWMDLAHTYFEIEAVNVSDLSPPARQVSNVNTTNOAASPVTNV 418
Qy 450 MKEVLORSVOLSWOEPHPNGVITEYIKTYEKDQRTYSTLTKSTASINLKPGT 509
Db 419 KKGIAKNSISLSMOEPRPNGIILEYIKHFEKQD-ETSYTIKSKETTTIAGLKRAS 477
Qy 510 VYVEFOIRAVTAAGYGNVSPRLDVAITLEBASGKMEAT---AVSSEONPVIITIAVAVAGT 566
Db 478 VYVFOIRARTAGYGVFSRFE-----FETTVFAASSDQSQIPVIAVSVTG- 525
Qy 567 IIVVMPFGPIGRHRCGYSKADQEGDEE-LYFHSLVNHLV 609
Db 526 VILLAVIAGVILSGRCGYSKAKODPEEKMHFH---NGHIKL 565
```

RESULT 10

```
US-10-732-923-13667
; Sequence 13667, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 13667
; LENGTH: 991
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-732-923-13667
```

Query Match 56.4%; Score 1829; DB 17; Length 991;

Best Local Similarity 57.4%; Pred. No. 7.9e-136;

Matches 348; Conservative 96; Mismatches 136; Indels 26; Gaps 9;

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Qy 8 PSW---IICVIMLGFAHTGEAQAKEYLLDSKAQOTLEWISSPPSGMEISGLDNY 65
Db 15 PGMTCLELCAALRSLASPG-----SEVNLDSRTVMGLMIAVPKMGWEIGEBVDNY 69
Qy 66 TPRTYQVQVMEPNONNMILRTNMISKGAQRIFEVLEKFTLRDCNSLPGLGTCKETENL 125
Db 70 APIHTYQVCKMEQNONNMILTSWISNGBRASPSELKFTLRDCNSLPGLGTCKETENM 129
Qy 126 YYYETDVTGNIRENLYVKIDITIADESFTQDGERKKMLNTEVREIPLSKKGFYLA 185
Db 130 YFFESDDEGDGNIRENOYIKIDITIADESFTELDGDVMLKLNTEVROVGLYTKGFIYA 189
Qy 186 FQDVGACIALVSVMYVYKCKWTIVENLAVFPDVTGSSFFSLVREKGVCS-SAESELEN 244
Db 190 FQDVGACIALVSVMYVYKCKPSVIRNLAIRPDTITGAASSQLLEVSGCVNHSVTDE-- 247
Qy 245 SPRNHCSEGEMLVPIGKCIKAGYQOKGDTCEPCGRFRYKSSODLQCSRPTHSFSDR 304
Db 248 -PKNHCSEGEMLVPIGKCIKAGYEEKNNTQYCRPEFPKASPHSPSCSCPHSYTLD 306
Qy 305 EGSSRCBCEDEGYRAPSDDPYVACTRPPSAPONTLEINQTTVSIEMSPADNGGRDVT 364
Db 307 EASTSCLEEYHYPRESDDPTMACTRPPSAPASISINNETSVLEWIPPADTGGRKDV 366
Qy 365 YRIICKRSMOEGECVPGSGNIGVMBQOTGEDNVYTMDLAHANTYFEVENVNVSVDL 424
Db 367 YRIICKRKNHSGLEACGSHVRILPQOTGLKNTSVWMDLAHTYFEIEAVNAGVSDQ 426
Qy 425 SRSORLFAVSIITGQAAPQVSGVMKEBVLORSVOLSWOEPHPNGVITEYIKYEKD 484
```

```
Db 427 NPGARQVSVVNTTNOAPSPVSSVKKGKITKNKISLSWOEPDRNGIILEYIKYEKD 486
Qy 485 QRETYSTIKTKSASAINNLKPGTVVFOIRATAAGYGNVSPRLDVAITLEBASGKME 544
Db 487 Q-ETSYTIKSKETTTIAGLKRASAVVFOIRATAAGYGVFSRFEET-----SP 537
Qy 545 ATAVERSEONPVIITIAVAVAGTIIIVFMVFGFIIRHRCGYSKADQEGDEE-LYFHSLV 603
Db 538 VLAASSDQSQIPIL-VVSVTVGIVLLAVIGFILSGRCGYSKAKODPEEKMHFH----- 592
Qy 604 NEHLV 609
Db 593 NGHIKL 598
```

RESULT 11

```
US-10-029-020-63
; Sequence 63, Application US/10029020
; Publication No. US2004003971A1
; GENERAL INFORMATION:
```

APPLICANT: Gangoli et al.

TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same

FILE REFERENCE: 21402-225

CURRENT APPLICATION NUMBER: US/10/029,020

PRIOR FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/256,704

PRIOR FILING DATE: 2000-12-19

PRIOR APPLICATION NUMBER: 60/311,590

PRIOR FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: 60/257,314

PRIOR FILING DATE: 2000-12-20

PRIOR APPLICATION NUMBER: 60/311,613

PRIOR FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: 60/315,617

PRIOR FILING DATE: 2001-08-29

PRIOR APPLICATION NUMBER: 60/307,506

PRIOR FILING DATE: 2001-07-24

PRIOR APPLICATION NUMBER: 60/322,358

PRIOR FILING DATE: 2001-09-14

PRIOR APPLICATION NUMBER: 60/294,075

PRIOR FILING DATE: 2001-05-29

PRIOR APPLICATION NUMBER: 60/288,153

PRIOR FILING DATE: 2001-05-02

NUMBER OF SEQ ID NOS: 190

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 63

LENGTH: 1005

TYPE: PRT

ORGANISM: Rattus norvegicus

US-10-029-020-63

Query Match 56.2%; Score 1821; DB 15; Length 1005;

Best Local Similarity 54.6%; Pred. No. 3.5e-135;

Matches 350; Conservative 97; Mismatches 138; Indels 56; Gaps 11;

```
Qy 6 RPSMIITLCY-----IW-----LLGFAHGEAQAKEYLLDSKAQOTLEWISSPSG 54
Db 25 RVPASLGGCSAPIKGPMTCLELCAALRSLASPSNEVNLDSRTVMGLMIAVFPKNG 84
Qy 55 WEESGLDENTYTPRTYQVQVMEPNONNMILRTNMISKGAQRIFEVLEKFTLRDCNSLP 114
Db 85 WEIEGVDENYAPPIHTYQVCKMEQNONNMILTSWISNGBRASFELKFTLRDCNSLP 144
Qy 115 VLGTCKETFNLYYYETDVTGNIRENLYVKIDITIADESFTQDGERKKMLNTEVREI 174
Db 145 GLGTCKETFNMYYYESDDEGNIRIKDQYIKIDITIADESFTELDGDVMLKLNTEV 204
Qy 175 GPLSKKGFYLAFOVVGACIALVSVMYVYKCKWTIVENLAVFPDVTGSSFFSLVREK 234
Db 205 GPLSKKGFYLAFOVVGACIALVSVMYVYKCKPSVIRNLAIRPDTITGAASSQLLEV 264
Qy 235 VSSAEBAENSPRNHCSEGEMLVPIGKCIKAGYQOKGDTCEPCGRFRYKSSODLQCS 294
```

```
Db 265 VN--HSVTDPPKMHCSAEGEMLVPIGKCMCKAGYEENKGTQYCRDPFKASPHSQTCS 322
Qy 295 RCPHSPDESGSSRCCEGDGYRAPSDPPVACTRPPSAPONLIENINQTVLSLEWSPADNGRNDV 354
Db 323 KCPHASTHBEASGSCCEKDYFRRESDDPPMACTRPPSAPRNAISNVNETSVLEMIIPP 382
Qy 355 ADNGRNDVYTRILCKKCSWEGCEVPCGSGNIGMPQOTGLEDNVYTMDLAHANYTPE 414
Db 383 ADTGGGKDVAYYILCKKCNHAGVCECGGHVRYLPQOIGLKNTSVMMADPLATNTYTFE 442
Qy 415 VEANGVSDLSRSGRLRAAVSITTCGAAPQVSGVMKERVLORSVOLSMOEPHPNVT 474
Db 443 IEANGVSDLSPTGRQVSVVNTTQAAPSPVTVKKGIAKNSISLSMOEPPRPNIGIL 502
Qy 475 EYEIKYEXDQERTYSTLTKTSTASINNLKPGTVYVFOIRAVTAAGYNSPRLDVAT 534
Db 503 EYEIKYEXKO-ETSYTIILSKETTITAEGLKPAVYVFOIRAVTAAGYVFSRRFE--- 558
Qy 535 LEEASGMFEATAV---SSQNPIIIVAVVAGTIIIVMVFGEIT-----GRR- 581
Db 559 -----FETTPVFGASNDOSQIPITIGSVTVGVIILAVMI-GFLLSGSCCEGCGGRAS 609
Qy 582 -----HCGYSKADQEGDE-LYFHSLVTNHLSV 609
Db 610 SLCAVAHPSLIWRCGYSKAKODPEERKHFFH---NGHKL 646
```

```
RESULT 12
US-10-316-124-3
; Sequence 3, Application US/10316124
; Publication No. US20030152574A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: METHODS AND COMPOSITIONS TO TREAT
; FILE REFERENCE: MFI01-291P1NM
; CURRENT APPLICATION NUMBER: US/10/316,124
; PRIORITY FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/339,995
; PRIORITY FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1037
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-316-124-3
```

```
Query Match 56.1%; Score 1819; DB 14; Length 1037;
Best Local Similarity 55.1%; Pred. No. 5.3e-135;
Matches 348; Conservative 98; Mismatches 134; Indels 52; Gaps 11;

Qy 6 RPSBW--IILCYIMLGFALTGEQAKEYLLDLSKAQOTLEWISSPSPGWEHISLDE 63
Db 37 RAPIMTCLLC-----AALPTLASPSNEVNLDSRTVMGDLGAIAPPKXGWEHIGVDE 91
Qy 64 NYTPIRTYOVCOVMEPNQNNMLRTNMTSKGNAORIFVELKFTLRDQNSLFGVGTCKETP 123
Db 92 NYAPIHYOVCKWEQONNNWLTSWSNEGASRIFELKFTLRDQNSLFGVGTCKETP 151
Qy 124 NLVYETDVTGNNIRENLVYKIDTIAADESFTQGDIGERRKMLNTEVRE IGPLSKKGFY 183
Db 152 NMYEFESDDQNGRIKENOYIKIDTIAADESFTELDIDGRVMKLNTEVRLVGPLSKKGFY 211
Qy 184 LAFODVACIALVSVKYYKKCWITVENLAVFPDTYVSGSESSLYVEKGYCVSAAEEAE 243
Db 212 LAFQDVACIALVSVRYKKCBVHLLAVFPDTTIGAGSSQLLEVSGCVN--HSVTD 269
Qy 244 NSPRMHCSAEGEMLVPIGKCIKAGYQOKGDTCEPCGRFRFYKSSODLQCSRCPYHSFD 303
Db 270 EPRKMHCSAEGEMLVPIGKCMCKAGYEENKGTQYCRDPFKASPHISQSGCKCPHSYTH 329
```

```
Qy 304 REGSSRCCEGDGYRAPSDPPVACTRPPSAPONLIENINQTVLSLEWSPADNGRNDV 353
Db 330 EEAESTCVCEKDYFRRESDDPPMACTRPPSAPRNAISNVNETSVLEMIIPADTGRKDV 389
Qy 364 TYIILCKRCSWEGCEVPCGSGNIGMPQOTGLEDNVYTMDLAHANYTPEVAVNVSD 423
Db 390 SYIACKKCNHAGVCECGGHVRYLPQOIGLKNTSVMMADPLATNTYTFEIAVGVSD 449
Qy 424 LSRGRLRAAVSITTCGAAPQVSGVMKERVLORSVOLSMOEPHPNVTYEIKYEXK 483
Db 450 LSPGAQVSVVNTTQAAPSPVTVKKGIAKNSISLSMOEPPRPNIGILEYIKHFEK 509
Qy 484 DQERTYSTLTKTSTASINNLKPGTVYVFOIRAVTAAGYNSPRLDVATLEEASGMF 543
Db 510 DQ-ETSYTIILSKETTITAEGLKPAVYVFOIRAVTAAGYVFSRRFE-----F 557
Qy 544 EAT---AVSEQNPVITIAVAVAGTIIIVMVFGEIT-----GRR----- 581
Db 558 ETPVFAASDQSLIVAVSVTVG-VILLAVIGVLSGSCCEGCGGRASLCAVAHPI 616
Qy 582 ---HCGYSKADQEGDE-LYFHSLVTNHLSV 609
Db 617 LWRGYSKAKODPEERKHFFH---NGHKL 644
```

```
RESULT 13
US-10-353-690-40
; Sequence 40, Application US/10353690
; Publication No. US20030215840A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Miyoung
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Healy, Aileen
; APPLICANT: Acton, Susan L.
; APPLICANT: Donoghue, Mary
; APPLICANT: Stagliano, Nancy
; APPLICANT: Redodin, Jacqueline
; APPLICANT: Rodrigue-Way, Amelie
; TITLE OF INVENTION: Methods and compositions for treating
; TITLE OF INVENTION: Cardiovascular disease using 1682, 6169, 6193, 7771, 14395,
; TITLE OF INVENTION: 29002, 33216, 43726, 69292, 26156, 32427, 2402, 7747, 11720,
; TITLE OF INVENTION: 9151, 60491, 1371, 7077, 33207, 1419, 18036, 16105, 38650,
; TITLE OF INVENTION: 14245, 58848, 1870, 25856, 32394, 3484, 345, 9252, 9135,
; TITLE OF INVENTION: 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912, 2868,
; TITLE OF INVENTION: 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914,
; TITLE OF INVENTION: 51130, 19489, 21833, 2917, 58590, 15992, 2094, 2252, 3474,
; TITLE OF INVENTION: 9792, 15400, 1452 OR 6585 molecules
; FILE REFERENCE: MFI02-018P1RQNM1M
; CURRENT APPLICATION NUMBER: US/10/353,690
; PRIORITY FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 60/353,224
; PRIORITY FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/364,529
; PRIORITY FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: 60/373,861
; PRIORITY FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/376,287
; PRIORITY FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 60/388,080
; PRIORITY FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: 60/390,971
; PRIORITY FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/394,130
; PRIORITY FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/394,797
; PRIORITY FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/404,904
; PRIORITY FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 60/405,450
; PRIORITY FILING DATE: 2002-08-23
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 126
```

SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 1037
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-353-690-40

Query Match 56.1%; Score 1819; DB 15; Length 1037;
Best Local Similarity 55.1%; Pred. No. 5.3e-135;
Matches 348; Conservative 98; Mismatches 134; Indels 52; Gaps 11;

```
QY 6 RFPBW--IILCYIMLGFPAHNGEAOAKVILLDSKAQOTLEWISSPPSGMEISGLDE 63
D 37 RAPLMTCLILC-----AALRTLLASPSNEVNLDSRTVMGDLGWIAPKMGMEIEGEYDE 91
QY 64 NYTPIRTYQCVQWEPNOMNLRTNMTSKGNAQRIFELEKFTLLDNCNLPVGLTCKET 123
D 92 NYAPIHTYQCKWEQONNMWLTSMISNEGASRIFELEKFTLLDNCNLPVGLTCKET 151
QY 124 NLYYETDYDTGRNIRENLVYKIDITIADESFTQDLGERMKLNTVEIREIGPLSKGFY 183
D 152 NMYYFESDDQNGRNIRENQYIKIDITIADESFTELDGRVMKLTVEIRDVGPLSKGFY 211
QY 184 LAFQDVACIALVSVKYYKKCWITVENLAVFPPTVTGSEFSSLYVRGTCVSSAEEBAE 243
D 212 LAFQDVACIALVSVRYKKCPSVRHIAVFPPITIGADSSQLLEVSGCVN--HSVTD 269
QY 244 NSPBMHCSAEGEMLVPIGKCIKAGYQOKGDTCEPCGRPFYKSSSODLQSCRPTHSFSD 303
D 270 EPPMHCSAEGEMLVPIGKCMCKAGYEKNGTCOVCRPFKASPHIOSCGKCPHSTYH 329
QY 304 REGSRCECEDGYRAPSDPPYVACTRPPSAPONLIFINOTVTSLEWSPPADNGGRNDV 363
D 330 EEAISTCVCEDYRRRESDPPTMACTRPPSAPRAISVNETSVLEWIPPADTGRNDV 389
QY 364 TYRILCRCSWEQECYPCGSNIGYMPQOTGLENNYTVMDLLAHANTFEVEAVNGYSD 423
D 390 SYTIACKCKNSHACVCECGGHVRYLPRQSLKNTSVMMVDLLAHNTYFIEIENVGSD 449
QY 424 LSRQRLFAAVSITTGQAAPSOVSGWMEKERVLORSVOLSNQEPHPNVCITVEYEIKYK 483
D 450 LSPBARQVSVNVTINQAAPSPVTNVKKGKIAKNSISLSWQEPHPNIIILEYEIKHEK 509
QY 484 DQERTYSTLKSTKSTASINNLKPGTVYVFOIRAVTAAGYGNVSPRLDVATLEBASGMF 543
D 510 DQ-ETSTYTIKSKETITTAEGLKPAASYVFOIRARTAGYGVFSRRFE-----F 557
QY 544 EAT---AVSSEQNVIILAAVAVAGTIIIVPMVFGFII-----GRR----- 581
D 558 ETTVFPAASDQSQIPVIAVSVTVG-VILLAVIGVLLSGSCBGGGRASSLCVAHP 616
QY 582 ---HGYSKADQEGDE-LYFHSLVTHNEHLSV 609
D 617 LIWRGYSKAKQDPEEKMHF---NGHITL 644
```

RESULT 14
US-11-064-551-3
; Sequence 3, Application US/11064551
; Publication No. US20050142604A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: METHODS AND COMPOSITIONS TO TREAT
; FILE REFERENCE: MP101-291PIRM
; CURRENT APPLICATION NUMBER: US/11/064,551
; PRIOR FILING DATE: 2005-02-24
; PRIOR APPLICATION NUMBER: 60/339,995
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3

LENGTH: 1037
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-064-551-3

Query Match 56.1%; Score 1819; DB 20; Length 1037;
Best Local Similarity 55.1%; Pred. No. 5.3e-135;
Matches 348; Conservative 98; Mismatches 134; Indels 52; Gaps 11;

```
QY 6 RFPBW--IILCYIMLGFPAHNGEAOAKVILLDSKAQOTLEWISSPPSGMEISGLDE 63
D 37 RAPLMTCLILC-----AALRTLLASPSNEVNLDSRTVMGDLGWIAPKMGMEIEGEYDE 91
QY 64 NYTPIRTYQCVQWEPNOMNLRTNMTSKGNAQRIFELEKFTLLDNCNLPVGLTCKET 123
D 92 NYAPIHTYQCKWEQONNMWLTSMISNEGASRIFELEKFTLLDNCNLPVGLTCKET 151
QY 124 NLYYETDYDTGRNIRENLVYKIDITIADESFTQDLGERMKLNTVEIREIGPLSKGFY 183
D 152 NMYYFESDDQNGRNIRENQYIKIDITIADESFTELDGRVMKLTVEIRDVGPLSKGFY 211
QY 184 LAFQDVACIALVSVKYYKKCWITVENLAVFPPTVTGSEFSSLYVRGTCVSSAEEBAE 243
D 212 LAFQDVACIALVSVRYKKCPSVRHIAVFPPITIGADSSQLLEVSGCVN--HSVTD 269
QY 244 NSPBMHCSAEGEMLVPIGKCIKAGYQOKGDTCEPCGRPFYKSSSODLQSCRPTHSFSD 303
D 270 EPPMHCSAEGEMLVPIGKCMCKAGYEKNGTCOVCRPFKASPHIOSCGKCPHSTYH 329
QY 304 REGSRCECEDGYRAPSDPPYVACTRPPSAPONLIFINOTVTSLEWSPPADNGGRNDV 363
D 330 EEAISTCVCEDYRRRESDPPTMACTRPPSAPRAISVNETSVLEWIPPADTGRNDV 389
QY 364 TYRILCRCSWEQECYPCGSNIGYMPQOTGLENNYTVMDLLAHANTFEVEAVNGYSD 423
D 390 SYTIACKCKNSHACVCECGGHVRYLPRQSLKNTSVMMVDLLAHNTYFIEIENVGSD 449
QY 424 LSRQRLFAAVSITTGQAAPSOVSGWMEKERVLORSVOLSNQEPHPNVCITVEYEIKYK 483
D 450 LSPBARQVSVNVTINQAAPSPVTNVKKGKIAKNSISLSWQEPHPNIIILEYEIKHEK 509
QY 484 DQERTYSTLKSTKSTASINNLKPGTVYVFOIRAVTAAGYGNVSPRLDVATLEBASGMF 543
D 510 DQ-ETSTYTIKSKETITTAEGLKPAASYVFOIRARTAGYGVFSRRFE-----F 557
QY 544 EAT---AVSSEQNVIILAAVAVAGTIIIVPMVFGFII-----GRR----- 581
D 558 ETTVFPAASDQSQIPVIAVSVTVG-VILLAVIGVLLSGSCBGGGRASSLCVAHP 616
QY 582 ---HGYSKADQEGDE-LYFHSLVTHNEHLSV 609
D 617 LIWRGYSKAKQDPEEKMHF---NGHITL 644
```

RESULT 15
US-10-412-277-8
; Sequence 8, Application US/10412277
; Publication No. US20030175791A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001067DIV
; CURRENT APPLICATION NUMBER: US/10/412,277
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 975
; TYPE: PRT
; ORGANISM: Human
US-10-412-277-8

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 23, 2005, 08:26:40 / Search time 21.2217 Seconds
(without alignments)
2145.727 Million cell updates/sec

Title: US-10-073-064-3
3243
Sequence: 1 MVQTRPPSWILCYMLG.....EGDELYFHSIVNEHLSVL 610

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|--------------------|
| 1 | 3243 | 100.0 | 610 | 3 | US-08-368-776A-3 |
| 2 | 3243 | 100.0 | 610 | 5 | PCT-US96-00419-3 |
| 3 | 3199 | 98.6 | 626 | 3 | US-08-368-776A-5 |
| 4 | 3199 | 98.6 | 626 | 5 | PCT-US96-00419-5 |
| 5 | 3192 | 98.4 | 994 | 3 | US-08-368-776A-12 |
| 6 | 3191 | 98.4 | 998 | 3 | US-08-368-776A-2 |
| 7 | 3191 | 98.4 | 998 | 5 | PCT-US96-00419-2 |
| 8 | 3151.5 | 97.2 | 993 | 3 | US-08-368-776A-11 |
| 9 | 3139 | 96.8 | 998 | 2 | US-08-449-645A-17 |
| 10 | 3139 | 96.8 | 998 | 2 | US-08-702-367A-17 |
| 11 | 3139 | 96.8 | 998 | 4 | US-09-949-016-6501 |
| 12 | 3139 | 96.8 | 998 | 5 | PCT-US95-04681-17 |
| 13 | 3139 | 96.8 | 1005 | 4 | US-09-949-016-9901 |
| 14 | 1843 | 56.8 | 991 | 2 | US-08-449-645A-13 |
| 15 | 1843 | 56.8 | 991 | 2 | US-08-702-367A-13 |
| 16 | 1843 | 56.8 | 991 | 5 | PCT-US95-04681-13 |
| 17 | 1835.5 | 56.6 | 967 | 2 | US-08-449-645A-30 |
| 18 | 1835.5 | 56.6 | 967 | 2 | US-08-702-367A-30 |
| 19 | 1832.5 | 56.5 | 953 | 4 | US-09-751-389-7 |
| 20 | 1824 | 56.2 | 1005 | 2 | US-08-469-537A-103 |
| 21 | 1808.5 | 55.8 | 975 | 4 | US-09-751-389-8 |
| 22 | 1793 | 55.3 | 983 | 1 | US-08-167-919A-10 |
| 23 | 1793 | 55.3 | 983 | 2 | US-08-449-645A-21 |
| 24 | 1793 | 55.3 | 983 | 2 | US-08-702-367A-21 |
| 25 | 1793 | 55.3 | 983 | 3 | US-08-715-106-10 |
| 26 | 1793 | 55.3 | 983 | 4 | US-09-442-649-10 |
| 27 | 1793 | 55.3 | 983 | 5 | PCT-US95-04681-21 |

| | | | | | | |
|----|--------|------|------|---|---------------------|--------------------|
| 28 | 1786.5 | 55.1 | 968 | 4 | US-09-751-389-6 | Sequence 6, Appli |
| 29 | 1778.5 | 54.8 | 983 | 1 | US-08-162-809-16 | Sequence 16, Appli |
| 30 | 1777 | 54.8 | 982 | 2 | US-08-673-789-4 | Sequence 4, Appli |
| 31 | 1736.5 | 53.5 | 986 | 2 | US-08-449-645A-15 | Sequence 15, Appli |
| 32 | 1736.5 | 53.5 | 986 | 2 | US-08-702-367A-15 | Sequence 15, Appli |
| 33 | 1736.5 | 53.5 | 986 | 5 | PCT-US95-04681-15 | Sequence 15, Appli |
| 34 | 1736.5 | 53.5 | 997 | 4 | US-09-949-016-7171 | Sequence 36, Appli |
| 35 | 1729.5 | 53.3 | 1104 | 1 | US-08-222-616-16 | Sequence 36, Appli |
| 36 | 1729.5 | 53.3 | 1104 | 3 | US-08-446-648-36 | Sequence 36, Appli |
| 37 | 1729.5 | 53.3 | 1104 | 4 | US-09-982-610-16 | Sequence 36, Appli |
| 38 | 1729.5 | 53.3 | 1104 | 5 | PCT-US95-04228-36 | Sequence 36, Appli |
| 39 | 1729 | 53.3 | 986 | 2 | US-08-673-789-3 | Sequence 3, Appli |
| 40 | 1701.5 | 52.5 | 1005 | 4 | US-09-949-016-6968 | Sequence 6968, Ap |
| 41 | 1701.5 | 52.5 | 1005 | 4 | US-09-949-016-10620 | Sequence 10620, A |
| 42 | 1670.5 | 51.5 | 1036 | 4 | US-09-751-389-2 | Sequence 2, Appli |
| 43 | 1666.5 | 51.4 | 942 | 4 | US-10-004-542-2 | Sequence 2, Appli |
| 44 | 1666.5 | 51.4 | 942 | 4 | US-10-430-797-2 | Sequence 2, Appli |
| 45 | 1662 | 51.2 | 948 | 2 | US-08-469-537A-101 | Sequence 101, App |

ALIGNMENTS

RESULT 1
US-08-368-776A-3
Sequence 3, Application US/08368776A
Patent No. 6300482
GENERAL INFORMATION:
APPLICANT: Closser, Thomas
APPLICANT: Ullrich, Axel
APPLICANT: Millauer, Birgit
TITLE OF INVENTION: METHODS FOR DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF MDK1
TITLE OF INVENTION: SIGNAL TRANSDUCTION
TITLE OF INVENTION: DISORDERS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESS: Lyon & Lyon
STREET: 633 West Filth Street
CITY: Suite 4700
STATE: California
CITY: Los Angeles
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/368, 776A
FILING DATE: January 3, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 610 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-368-776A-3

Query Match 100.0%; Score 3243; DB 3; Length 610;
Best Local Similarity 100.0%; Pred. No. 4.7e-294;
Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MVTQTRPPSWIILCYIWLGFHAGTGEAQAKEYLLDSKAQOTLEWISS:PSGMEIISG 60
DB 1 MVTQTRPPSWIILCYIWLGFHAGTGEAQAKEYLLDSKAQOTLEWISS:PSGMEIISG 60
QY 61 LDENVTPIRTYQVCOVMEPNQNNMLRTNMSKGAQRIFVELKFTLRDNCSLPGVGTCK 120
DB 61 LDENVTPIRTYQVCOVMEPNQNNMLRTNMSKGAQRIFVELKFTLRDNCSLPGVGTCK 120
QY 121 EFNLYYYETDYGGRINRENLVYKIDTIAADESFTQGLGERKMKLNTREIGPLSKK 180
DB 121 EFNLYYYETDYGGRINRENLVYKIDTIAADESFTQGLGERKMKLNTREIGPLSKK 180
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DB 181 GFYLAFOVDGACIALVSVKYYKKCWTIVENLAVFPDVTGSEFSSLVEVAGTCVSSAEE 240
QY 241 EAENSPRMHCSAEGEWLVPIGKCTCKAGYQOKGDTCEPCGRPFYKSSSODLQCSRCPHIS 300
DB 241 EAENSPRMHCSAEGEWLVPIGKCTCKAGYQOKGDTCEPCGRPFYKSSSODLQCSRCPHIS 300
QY 301 FSDREGSSRCCEDEGYRAPSDEPPYVACTRPPSAPQNLFININQTVSLSEMPADNGGR 360
DB 301 FSDREGSSRCCEDEGYRAPSDEPPYVACTRPPSAPQNLFININQTVSLSEMPADNGGR 360
QY 361 NDVTYRILCKRCGMEGECVPCGSNIGYMPQOTGLENDYVTVMDLLAHANYTPEVAANG 420
DB 361 NDVTYRILCKRCGMEGECVPCGSNIGYMPQOTGLENDYVTVMDLLAHANYTPEVAANG 420
QY 421 VSDLSRSORLFAVSIITGGAAPSOVSGWKEKRLQRSVQLSQOEPEHNGVITEYIKY 480
DB 421 VSDLSRSORLFAVSIITGGAAPSOVSGWKEKRLQRSVQLSQOEPEHNGVITEYIKY 480
QY 481 YEKDQERTYSTLTKTSTASINNLKPGTVYFQIRAVTAAGYGNYSPLDVALTEBASG 540
DB 481 YEKDQERTYSTLTKTSTASINNLKPGTVYFQIRAVTAAGYGNYSPLDVALTEBASG 540
QY 541 KMFATAVSSQNPVITIIAVVAVAGTIIIVFVFGFIIIGRRHCGYSKADCEGBELYFHS 600
DB 541 KMFATAVSSQNPVITIIAVVAVAGTIIIVFVFGFIIIGRRHCGYSKADCEGBELYFHS 600
QY 601 LVTNEHLSVL 610
DB 601 LVTNEHLSVL 610

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RESULT 2 PCT-US96-00419-3

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: Sequence 3, Application PC/TUS9600419
: GENERAL INFORMATION:
: APPLICANT: Thomas Ciosek, Axel Ulrich, Birgit
: APPLICANT: Millauer
: TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF
: TITLE OF INVENTION: MDK1 SIGNAL TRANSDUCTION DISORDERS
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Lyon & Lyon
: STREET: 633 West Fifth Street
: CITY: Los Angeles
: STATE: California
: COUNTRY: USA
: ZIP: 90071
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
: COMPUTER: IBM compatible
: OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
: SOFTWARE: WordPerfect (Version 5.1)

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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US96/00419
: FILING DATE: January 3, 1995
: CLASSIFICATION:
: PRIOR APPLICATION DATA: including application
: PRIOR APPLICATION DATA: described below: none
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Warburg, Richard J.
: REGISTRATION NUMBER: 32,327
: REFERENCE/DOCKET NUMBER: 208/007
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (213) 489-1600
: TELEFAX: (213) 955-0440
: TELEX: 67-3510
: INFORMATION FOR SEQ. ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 610
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: PCT-US96-00419-3

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Query Match 100.0%; Score 3243; DB 5; Length 610;
Best Local Similarity 100.0%; Pred. No. 4.7e-294;
Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MVTQTRPPSWIILCYIWLGFHAGTGEAQAKEYLLDSKAQOTLEWISS:PSGMEIISG 60
DB 1 MVTQTRPPSWIILCYIWLGFHAGTGEAQAKEYLLDSKAQOTLEWISS:PSGMEIISG 60
QY 61 LDENVTPIRTYQVCOVMEPNQNNMLRTNMSKGAQRIFVELKFTLRDNCSLPGVGTCK 120
DB 61 LDENVTPIRTYQVCOVMEPNQNNMLRTNMSKGAQRIFVELKFTLRDNCSLPGVGTCK 120
QY 121 EFNLYYYETDYGGRINRENLVYKIDTIAADESFTQGLGERKMKLNTREIGPLSKK 180
DB 121 EFNLYYYETDYGGRINRENLVYKIDTIAADESFTQGLGERKMKLNTREIGPLSKK 180
QY 181 GFYLAFOVDGACIALVSVKYYKKCWTIVENLAVFPDVTGSEFSSLVEVAGTCVSSAEE 240
DB 181 GFYLAFOVDGACIALVSVKYYKKCWTIVENLAVFPDVTGSEFSSLVEVAGTCVSSAEE 240
QY 241 EAENSPRMHCSAEGEWLVPIGKCTCKAGYQOKGDTCEPCGRPFYKSSSODLQCSRCPHIS 300
DB 241 EAENSPRMHCSAEGEWLVPIGKCTCKAGYQOKGDTCEPCGRPFYKSSSODLQCSRCPHIS 300
QY 301 FSDREGSSRCCEDEGYRAPSDEPPYVACTRPPSAPQNLFININQTVSLSEMPADNGGR 360
DB 301 FSDREGSSRCCEDEGYRAPSDEPPYVACTRPPSAPQNLFININQTVSLSEMPADNGGR 360
QY 361 NDVTYRILCKRCGMEGECVPCGSNIGYMPQOTGLENDYVTVMDLLAHANYTPEVAANG 420
DB 361 NDVTYRILCKRCGMEGECVPCGSNIGYMPQOTGLENDYVTVMDLLAHANYTPEVAANG 420
QY 421 VSDLSRSORLFAVSIITGGAAPSOVSGWKEKRLQRSVQLSQOEPEHNGVITEYIKY 480
DB 421 VSDLSRSORLFAVSIITGGAAPSOVSGWKEKRLQRSVQLSQOEPEHNGVITEYIKY 480
QY 481 YEKDQERTYSTLTKTSTASINNLKPGTVYFQIRAVTAAGYGNYSPLDVALTEBASG 540
DB 481 YEKDQERTYSTLTKTSTASINNLKPGTVYFQIRAVTAAGYGNYSPLDVALTEBASG 540
QY 541 KMFATAVSSQNPVITIIAVVAVAGTIIIVFVFGFIIIGRRHCGYSKADCEGBELYFHS 600
DB 541 KMFATAVSSQNPVITIIAVVAVAGTIIIVFVFGFIIIGRRHCGYSKADCEGBELYFHS 600
QY 601 LVTNEHLSVL 610
DB 601 LVTNEHLSVL 610

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RESULT 3

US-08-368-776A-5

Sequence 5, Application US/08368776A

Patent No. 6300482

GENERAL INFORMATION:

APPLICANT: Ciosek, Thomas

APPLICANT: Ullrich, Axel

APPLICANT: Millaer, Birgit

TITLE OF INVENTION: METHODS FOR DIAGNOSIS

TITLE OF INVENTION: AND TREATMENT OF MDX1

TITLE OF INVENTION: SIGNAL TRANSDUCTION

TITLE OF INVENTION: DISORDERS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESS: Lyon & Lyon Street

STREET: 633 West Filth Street

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/368,776A

FILING DATE: January 3, 1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including application

APPLICATION NUMBER: described below: none

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 208/007

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 626 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-368-776A-5

Query Match 98.6%; Score 3199; DB 3; Length 626;
Best Local Similarity 100.0%; Pred. No. 6.3e-290;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVOGTRPSPWILLCYIWLGFAGTGEAQAQAVILLDSKAQOTELWISSPPSGMEEISG 60
DB 1 MVOGTRPSPWILLCYIWLGFAGTGEAQAQAVILLDSKAQOTELWISSPPSGMEEISG 60
QY 61 LDENVTPRTYOVQWEPNPNMRLRTWISKNAQRIFVFLKFTLRDNCNLPGLGTCK 120
DB 61 LDENVTPRTYOVQWEPNPNMRLRTWISKNAQRIFVFLKFTLRDNCNLPGLGTCK 120
QY 121 ETFNLVYETDYDGRNIRENLVYKIDTIADESFTQDGLGRKKKAKTEVREIGPLSKK 180
DB 121 ETFNLVYETDYDGRNIRENLVYKIDTIADESFTQDGLGRKKKAKTEVREIGPLSKK 180
QY 181 GFYLAFOVGAACIALVSVKYYKKCWTIVENLAVPDTVTGSSEFSLVEVGTGVSSAEE 240
DB 181 GFYLAFOVGAACIALVSVKYYKKCWTIVENLAVPDTVTGSSEFSLVEVGTGVSSAEE 240

DB 181 GFYLAFOVGAACIALVSVKYYKKCWTIVENLAVPDTVTGSSEFSLVEVGTGVSSAEE 240
QY 241 EAENSPPMHCSABGEMLVPIGKCIKAGYQOKGPTCEGRRPFYKSSODLQSCRCPHHS 300
DB 241 EAENSPPMHCSABGEMLVPIGKCIKAGYQOKGPTCEGRRPFYKSSODLQSCRCPHHS 300
QY 301 FSDREGSSRCEDGYRAPSDPPYACTRPPSAQNLIFINQTVTSLEWSPADNGR 360
DB 301 FSDREGSSRCEDGYRAPSDPPYACTRPPSAQNLIFINQTVTSLEWSPADNGR 360
QY 361 NDVYTRILCRCSMEQECVPCSGNIGYMPQGTGLENNYVMDLLAHANTFEVAVNG 420
DB 361 NDVYTRILCRCSMEQECVPCSGNIGYMPQGTGLENNYVMDLLAHANTFEVAVNG 420
QY 421 VSDLSRQRLFAAVSITGGAAPSOVSGWKKERYLQSVOLSMQEPHPNGVITEYIKY 480
DB 421 VSDLSRQRLFAAVSITGGAAPSOVSGWKKERYLQSVOLSMQEPHPNGVITEYIKY 480
QY 481 YEKQRRRTYSTLKSTKSASINNLKPGTYVFOIRAVTAAGYGNYSPLDVATLEASG 540
DB 481 YEKQRRRTYSTLKSTKSASINNLKPGTYVFOIRAVTAAGYGNYSPLDVATLEASG 540
QY 541 KMFETAVSSQONPVIIIAVAVAGTIIIVPMVGFIIGRHCGYSTADQDEBELYFHS 600
DB 541 KMFETAVSSQONPVIIIAVAVAGTIIIVPMVGFIIGRHCGYSTADQDEBELYFHS 600
QY 601 L 601
DB 601 L 601

RESULT 4

PCT-US96-00419-5

Sequence 5, Application PC/TUS9600419

GENERAL INFORMATION:

APPLICANT: Thomas Ciosek, Axel Ullrich, Birgit

APPLICANT: Millaer

TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF

TITLE OF INVENTION: MDX1 SIGNAL TRANSDUCTION DISORDERS

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESS: Lyon & Lyon

STREET: 633 West Filth Street

CITY: Los Angeles

STATE: California

COUNTRY: USA

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM compatible

OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)

SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/00419

FILING DATE: January 3, 1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including application

APPLICATION NUMBER: described below: none

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 208/007

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 626

TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-00419-5

Query Match 98.6%; Score 3199; DB 5; Length 624;
Best Local Similarity 100.0%; Pred. No. 6.3e-290;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MVOVTRPSPWIIICYIMLGFATGGAQAQAEVLLDLSKAQOTLEWISSPPSGWEIISG 60
DB 1 MVOVTRPSPWIIICYIMLGFATGGAQAQAEVLLDLSKAQOTLEWISSPPSGWEIISG 60
QY 61 LDENVYPIRTYQVCQVMEPNQNNMLRTNWSKGAQRI FVELKFTLRDCNSLPGLGTCK 120
DB 61 LDENVYPIRTYQVCQVMEPNQNNMLRTNWSKGAQRI FVELKFTLRDCNSLPGLGTCK 120
QY 121 ETFNLVYETDYPYGNIRRENLVYKIDTIAADESFTQDGERKMKLNTVEIREIGPLSKK 180
DB 121 ETFNLVYETDYPYGNIRRENLVYKIDTIAADESFTQDGERKMKLNTVEIREIGPLSKK 180
QY 181 GFYLAFOVDGACIALVSVKYKCKMTIYENLAVFPDVTGSEFSSLVEVRGTCVSSAEE 240
DB 181 GFYLAFOVDGACIALVSVKYKCKMTIYENLAVFPDVTGSEFSSLVEVRGTCVSSAEE 240
QY 241 EAENSPRMHCSAEGEWLVPIGKCIKAGYQOKGDTCEPCGRPFYKSSODLQCSRPTHS 300
DB 241 EAENSPRMHCSAEGEWLVPIGKCIKAGYQOKGDTCEPCGRPFYKSSODLQCSRPTHS 300
QY 301 FSDREGSSRCCEGYYRAPSDPPYVACTRPPAPQNLIFINQTTVSLWSPADNGGR 360
DB 301 FSDREGSSRCCEGYYRAPSDPPYVACTRPPAPQNLIFINQTTVSLWSPADNGGR 360
QY 361 NDVTYRILCKRCSEWEGECVPCGSNIGMPQOTGLBNYTVMDLAAHYTFPEVAVNG 420
DB 361 NDVTYRILCKRCSEWEGECVPCGSNIGMPQOTGLBNYTVMDLAAHYTFPEVAVNG 420
QY 421 VSDLSRSQRLFAAVSITTTGAAPSQVSGVWKERVLSQVLSQWEPHPHGVITEYEIKY 480
DB 421 VSDLSRSQRLFAAVSITTTGAAPSQVSGVWKERVLSQVLSQWEPHPHGVITEYEIKY 480
QY 481 YEKDQREERTYTLTKTSTASINNLKPGTYVYFOIRAVTAAGYNSPRLDVAITLEASG 540
DB 481 YEKDQREERTYTLTKTSTASINNLKPGTYVYFOIRAVTAAGYNSPRLDVAITLEASG 540
QY 541 KMFPAATVSSQONVITIAVAVAGTIIIVMVGFTIIGRRHCGYSADQEGDELYFHS 600
DB 541 KMFPAATVSSQONVITIAVAVAGTIIIVMVGFTIIGRRHCGYSADQEGDELYFHS 600
QY 601 L 601
DB 601 L 601

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RESULT 5
US-08-368-776A-12
Sequence 12, Application US/08368776A
Patent No. 6300482

GENERAL INFORMATION:
APPLICANT: Ciosek, Thomas
APPLICANT: Ullrich, Axel
APPLICANT: Millauer, Birgit
TITLE OF INVENTION: METHODS FOR DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF MDK1
TITLE OF INVENTION: SIGNAL TRANSDUCTION
TITLE OF INVENTION: DISORDERS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California

COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/368,776A
FILING DATE: January 3, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 994 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-368-776A-12

Query Match 98.4%; Score 3192; DB 3; Length 994;
Best Local Similarity 99.5%; Pred. No. 5.9e-289;
Matches 600; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 MVOVTRPSPWIIICYIMLGFATGGAQAQAEVLLDLSKAQOTLEWISSPPSGWEIISG 60
DB 1 MVOVTRPSPWIIICYIMLGFATGGAQAQAEVLLDLSKAQOTLEWISSPPSGWEIISG 60
QY 61 LDENVYPIRTYQVCQVMEPNQNNMLRTNWSKGAQRI FVELKFTLRDCNSLPGLGTCK 120
DB 61 LDENVYPIRTYQVCQVMEPNQNNMLRTNWSKGAQRI FVELKFTLRDCNSLPGLGTCK 120
QY 121 ETFNLVYETDYPYGNIRRENLVYKIDTIAADESFTQDGERKMKLNTVEIREIGPLSKK 180
DB 121 ETFNLVYETDYPYGNIRRENLVYKIDTIAADESFTQDGERKMKLNTVEIREIGPLSKK 180
QY 181 GFYLAFOVDGACIALVSVKYKCKMTIYENLAVFPDVTGSEFSSLVEVRGTCVSSAEE 240
DB 181 GFYLAFOVDGACIALVSVKYKCKMTIYENLAVFPDVTGSEFSSLVEVRGTCVSSAEE 240
QY 241 EAENSPRMHCSAEGEWLVPIGKCIKAGYQOKGDTCEPCGRPFYKSSODLQCSRPTHS 300
DB 241 EAENSPRMHCSAEGEWLVPIGKCIKAGYQOKGDTCEPCGRPFYKSSODLQCSRPTHS 300
QY 301 FSDREGSSRCCEGYYRAPSDPPYVACTRPPAPQNLIFINQTTVSLWSPADNGGR 360
DB 301 FSDREGSSRCCEGYYRAPSDPPYVACTRPPAPQNLIFINQTTVSLWSPADNGGR 360
QY 361 NDVTYRILCKRCSEWEGECVPCGSNIGMPQOTGLBNYTVMDLAAHYTFPEVAVNG 420
DB 361 NDVTYRILCKRCSEWEGECVPCGSNIGMPQOTGLBNYTVMDLAAHYTFPEVAVNG 420
QY 421 VSDLSRSQRLFAAVSITTTGAAPSQVSGVWKERVLSQVLSQWEPHPHGVITEYEIKY 480
DB 421 VSDLSRSQRLFAAVSITTTGAAPSQVSGVWKERVLSQVLSQWEPHPHGVITEYEIKY 480
QY 481 YEKDQREERTYTLTKTSTASINNLKPGTYVYFOIRAVTAAGYNSPRLDVAITLEASG 540
DB 481 YEKDQREERTYTLTKTSTASINNLKPGTYVYFOIRAVTAAGYNSPRLDVAITLEASG 540

```

Qy 541 KMFEATAVSSSEONVITIIA VAVAGTIIIVFMVFGFIIGRRHCGYSKADQGBDELYFHS 600
Db 541 KMFEATAVSSSEONVITIIA VAVAGTIIIVFMVFGFIIGRRHCGYSKADQGBDELYFHS 600

Qy 601 LVT 603
Db 601 TKT 603

RESULT 6
US-08-368-776A-2
; Sequence 2, Application US/08368776A
; Patent No. 6300482

GENERAL INFORMATION:
APPLICANT: Ciosek, Thomas
APPLICANT: Ulrich, Axel
APPLICANT: Millaer, Birgit
TITLE OF INVENTION: METHODS FOR DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF MDK1
TITLE OF INVENTION: SIGNAL TRANSDUCTION
TITLE OF INVENTION: DISORDERS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/368,776A
FILING DATE: January 3, 1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: none
APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:
NAME: Wardburg, Richard J.
REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 208/007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 998 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-368-776A-2

Query Match 98.4%; Score 3191; DB 3; Length 998;
Best Local Similarity 100.0%; Pred. No. 7,4e-289;
Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MVTGTRPSPWIIICVIMLGFAGTGEAQAKEVLLDSKAQOTLEWISSPPSGMEETISG 60
Db 1 MVTGTRPSPWIIICVIMLGFAGTGEAQAKEVLLDSKAQOTLEWISSPPSGMEETISG 60
Qy 61 LDENVTPIRTYQVCQVNEPNNMLRTNWSKGAORI FVELKFTLRDCNSLPVGLGTCK 120
Db 61 LDENVTPIRTYQVCQVNEPNNMLRTNWSKGAORI FVELKFTLRDCNSLPVGLGTCK 120

Db 61 LDENVTPIRTYQVCQVNEPNNMLRTNWSKGAORI FVELKFTLRDCNSLPVGLGTCK 120
Qy 121 ETPNLYYYETDPDYGRIINRENLVYKIDITIADESFOTGDLGERMKANTREIRIGPSKK 180
Db 121 ETPNLYYYETDPDYGRIINRENLVYKIDITIADESFOTGDLGERMKANTREIRIGPSKK 180
Qy 181 GFYLAPODVAGACIALVSKYKYKWCMTIVENLA VFPDVTGSEFSSLVEVAGTCVSSAEE 240
Db 181 GFYLAPODVAGACIALVSKYKYKWCMTIVENLA VFPDVTGSEFSSLVEVAGTCVSSAEE 240
Qy 241 EAENSPRMHCSABEEMLVPIGKCI CKAGYQOKGTCPCGRRFPYKSSSODLQCRCTHS 300
Db 241 EAENSPRMHCSABEEMLVPIGKCI CKAGYQOKGTCPCGRRFPYKSSSODLQCRCTHS 300
Qy 301 FSDREGSSRCECEGYRAPSDPPYVACTRPPSAPOULFININOTTVSLEKSPPADNGR 360
Db 301 FSDREGSSRCECEGYRAPSDPPYVACTRPPSAPOULFININOTTVSLEKSPPADNGR 360
Qy 361 NDVYRIILCKRCSWEQECVPCGSNIGMPQOTGLIEDNYVTYMDL LAHANYTFEVAANG 420
Db 361 NDVYRIILCKRCSWEQECVPCGSNIGMPQOTGLIEDNYVTYMDL LAHANYTFEVAANG 420
Qy 421 VSDLSRQRLFAVSIITGQAAPSQVGVKMERVLQSRVOLSQEPHPNGVITTEYIKY 480
Db 421 VSDLSRQRLFAVSIITGQAAPSQVGVKMERVLQSRVOLSQEPHPNGVITTEYIKY 480
Qy 481 YEKQREERTYSLTKTSTASINNLKPGTYVFOIRAVTAAGVNSPRLDVALTEASG 540
Db 481 YEKQREERTYSLTKTSTASINNLKPGTYVFOIRAVTAAGVNSPRLDVALTEASG 540
Qy 541 KMFEATAVSSSEONVITIIA VAVAGTIIIVFMVFGFIIGRRHCGYSKADQGBDELYFHS 599
Db 541 KMFEATAVSSSEONVITIIA VAVAGTIIIVFMVFGFIIGRRHCGYSKADQGBDELYFHS 599

RESULT 7

PCT-US96-00419-2
; Sequence 2, Application PC/TUS9600419

GENERAL INFORMATION:

APPLICANT: Thomas Ciosek, Axel Ulrich, Birgit
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: MDK1 SIGNAL TRANSDUCTION DISORDERS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00419
FILING DATE: January 3, 1995
CLASSIFICATION:

PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: none
APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:
NAME: Wardburg, Richard J.
REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 208/007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440

Qy 61 LDENVTPIRTYQVCQVNEPNNMLRTNWSKGAORI FVELKFTLRDCNSLPVGLGTCK 120
Db 61 LDENVTPIRTYQVCQVNEPNNMLRTNWSKGAORI FVELKFTLRDCNSLPVGLGTCK 120

; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 998
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; PCT: US96-00419-2

Query Match 98.4%; Score 3191; DB 5; Length 998;
 Best Local Similarity 100.0%; Pred. No. 7, 4e-289;
 Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVVQTRFSPSWIILCYIMLGFATGEOAAKEVILLDSKAAQTELEMISSPSGMEISG 60
 DB 1 MVVQTRFSPSWIILCYIMLGFATGEOAAKEVILLDSKAAQTELEMISSPSGMEISG 60
 QY 61 LDENVTPIRTYQVQVMEPNQNNMLRTNWSKNAQRIPELKTLLDCKNLPGVLTGCK 120
 DB 61 LDENVTPIRTYQVQVMEPNQNNMLRTNWSKNAQRIPELKTLLDCKNLPGVLTGCK 120
 QY 121 EFTNLVYETDVTGKRIENLYVKIDITIADESFTQDGERKMLNTEVREIGPLSKK 180
 DB 121 EFTNLVYETDVTGKRIENLYVKIDITIADESFTQDGERKMLNTEVREIGPLSKK 180
 QY 181 GFYLAFQDVACIALVSVKYKKKWTIVENLAVPDVTGSEFSSLVEVKGTCVSSABE 240
 DB 181 GFYLAFQDVACIALVSVKYKKKWTIVENLAVPDVTGSEFSSLVEVKGTCVSSABE 240
 QY 241 EAENSPRMHCSAEGEWLVPFGKICAKAGYQOKGDTCEPGRRFPKSSODLQSCRPTHS 300
 DB 241 EAENSPRMHCSAEGEWLVPFGKICAKAGYQOKGDTCEPGRRFPKSSODLQSCRPTHS 300
 QY 301 FSDREGSSRCECDGYRRAPSDPPYVACTRPPSAPQNLFININQTVLSLESPPADNGR 360
 DB 301 FSDREGSSRCECDGYRRAPSDPPYVACTRPPSAPQNLFININQTVLSLESPPADNGR 360
 QY 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQQTGLDENVYTVMDLLAHANFTFEVEAVNG 420
 DB 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQQTGLDENVYTVMDLLAHANFTFEVEAVNG 420
 QY 421 VSDLSRSQRLFAAVSITTTGQAPSOVGVKMERVLQRSVQSWQEPHPN3VITEYEIKY 480
 DB 421 VSDLSRSQRLFAAVSITTTGQAPSOVGVKMERVLQRSVQSWQEPHPN3VITEYEIKY 480
 QY 481 YEKDQERTYSTLTKTSTASINNLKPGTYVFOIRAVTAAGYGNYSRPLDVAITLEASG 540
 DB 481 YEKDQERTYSTLTKTSTASINNLKPGTYVFOIRAVTAAGYGNYSRPLDVAITLEASG 540
 QY 541 KMFEPATVSSQONFVILIAVAVAGTILVFMVFGFIIGRRHCGYSKADQEGDELYFH 599
 DB 541 KMFEPATVSSQONFVILIAVAVAGTILVFMVFGFIIGRRHCGYSKADQEGDELYFH 599

RESULT 8
 US-08-368-776A-11
 ; Sequence 11, Application US/08368776A
 ; Patent No. 6300482

; GENERAL INFORMATION:
 ; APPLICANT: Ciossek, Thomas
 ; APPLICANT: Ulrich, Axel
 ; APPLICANT: Mullauer, Birgit
 ; TITLE OF INVENTION: METHODS FOR DIAGNOSIS
 ; TITLE OF INVENTION: AND TREATMENT OF MDK1
 ; TITLE OF INVENTION: SIGNAL TRANSDUCTION
 ; NUMBER OF INVENTION: DISORDERS
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; STREET: Suite 4700
 ; CITY: Los Angeles
 ; STATE: California

; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/368, 776A
 ; FILING DATE: January 3, 1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; PRIOR APPLICATION DATA: including application
 ; PRIOR APPLICATION DATA: described below: none
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 208/007
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 993 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-368-776A-11

Query Match 97.2%; Score 3151.5; DB 3; Length 993;
 Best Local Similarity 99.2%; Pred. No. 3, 6e-285;
 Matches 594; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 1 MVVQTRFSPSWIILCYIMLGFATGEOAAKEVILLDSKAAQTELEMISSPSGMEISG 60
 DB 1 MVVQTRFSPSWIILCYIMLGFATGEOAAKEVILLDSKAAQTELEMISSPSGMEISG 60
 QY 61 LDENVTPIRTYQVQVMEPNQNNMLRTNWSKNAQRIPELKTLLDCKNLPGVLTGCK 120
 DB 61 LDENVTPIRTYQVQVMEPNQNNMLRTNWSKNAQRIPELKTLLDCKNLPGVLTGCK 120
 QY 121 EFTNLVYETDVTGKRIENLYVKIDITIADESFTQDGERKMLNTEVREIGPLSKK 180
 DB 121 EFTNLVYETDVTGKRIENLYVKIDITIADESFTQDGERKMLNTEVREIGPLSKK 180
 QY 181 GFYLAFQDVACIALVSVKYKKKWTIVENLAVPDVTGSEFSSLVEVKGTCVSSABE 240
 DB 181 GFYLAFQDVACIALVSVKYKKKWTIVENLAVPDVTGSEFSSLVEVKGTCVSSABE 240
 QY 241 EAENSPRMHCSAEGEWLVPFGKICAKAGYQOKGDTCEPGRRFPKSSODLQSCRPTHS 300
 DB 241 EAENSPRMHCSAEGEWLVPFGKICAKAGYQOKGDTCEPGRRFPKSSODLQSCRPTHS 300
 QY 301 FSDREGSSRCECDGYRRAPSDPPYVACTRPPSAPQNLFININQTVLSLESPPADNGR 360
 DB 301 FSDREGSSRCECDGYRRAPSDPPYVACTRPPSAPQNLFININQTVLSLESPPADNGR 360
 QY 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQQTGLDENVYTVMDLLAHANFTFEVEAVNG 420
 DB 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQQTGLDENVYTVMDLLAHANFTFEVEAVNG 420
 QY 421 VSDLSRSQRLFAAVSITTTGQAPSOVGVKMERVLQRSVQSWQEPHPN3VITEYEIKY 480
 DB 421 VSDLSRSQRLFAAVSITTTGQAPSOVGVKMERVLQRSVQSWQEPHPN3VITEYEIKY 480
 QY 481 YEKDQERTYSTLTKTSTASINNLKPGTYVFOIRAVTAAGYGNYSRPLDVAITLEASG 540
 DB 481 YEKDQERTYSTLTKTSTASINNLKPGTYVFOIRAVTAAGYGNYSRPLDVAITLEASG 540

| | | | |
|----|-----|---|------|
| Qy | 244 | EAEKSPRMHCSAGCEMLVIGKICIKAGYQQAQGDPCCECGRRFPYXSSSDQJQCRCTHS | 3000 |
| Db | 241 | EAEKAPRMHCSAGCEMLVIGKICIKAGYQQAQGDPCCECGRRFPYXSSSDQJQCRCTHS | 3000 |
| Qy | 301 | FSDREGSSRCECEGDYYRAPSDPYPYACTRPPSAQNLIFININQTTWSLEMSPADNCGR | 3600 |
| Db | 301 | FSDREGSSRCECEGDYYRAPSDPYPYACTRPPSAQNLIFININQTTWSLEMSPADNCGR | 3600 |
| Qy | 361 | NDVTYRILCKRCGMEQGCVPCCGSNIGYMPQDTGEDNYVTYMDLAAHYTFEEVAVNG | 4200 |
| Db | 361 | NDVTYRILCKRCGMEQGCVPCCGSNIGYMPQDTGEDNYVTYMDLAAHYTFEEVAVNG | 4200 |
| Qy | 421 | VSDLSRSORLFAAVSITTTQAAAPSOYGVGMKERVQORSVQJLSMOEPHNGVITYEIKY | 4800 |
| Db | 421 | VSDLSRSORLFAAVSITTTQAAAPSOYGVGMKERVQORSVQJLSMOEPHNGVITYEIKY | 4800 |
| Qy | 481 | YKEDQERRYSLTKTSTASISNNLKPGVNVYFOIRATTAAGYGVSPRLDVAATLEASG | 5400 |
| Db | 481 | YKEDQERRYSLTKTSTASISNNLKPGVNVYFOIRATTAAGYGVSPRLDVAATLEASG | 5400 |
| Qy | 541 | KMEFARAVSSEQPVLIIIVAVAGTIIIVFWFGIIGRRHCGYSKADQGDDELFTFH | 599 |
| Db | 541 | KMEFARAVSSEQPVLIIIVAVAGTIIIVFWFGIIGRRHCGYSKADQGDDELFTFH | 599 |

```

RESULT 13
US-09-949-016-9901
: Sequence 9901, Application US/09949016
: Patent No. 6812339
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: C1001307
: CURRENT APPLICATION NUMBER: US/09/949, 016
: CURRENT FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 9901
: LENGTH: 1005
: TYPE: PRT
: ORGANISM: Human
: US-09-949-016-9901

```

| | Query Match | 96.8% | Score 3139 | DB 4 | Length 1005 |
|----|-----------------------|---|--------------------|----------|-------------|
| | Best Local Similarity | 97.7% | Pred. No. 5.4e-284 | | |
| | Matches 585 | Conservative 10 | Mismatches 4 | Indels 0 | Gaps 0 |
| Qy | 1 | MVVQTRPSPWIIICIMWLGFAHTGEAQAAREVLLDSKAAQTELEWISSPSPGWEIISG | 60 | | |
| Dd | 8 | MVFQTRPSPWIIICIMWLRFAHTGEAQAAREVLLDSKAAQTELEWISSPSPNGWEIISG | 67 | | |
| Qy | 61 | LDENVYTPRTTYQVCQWMEPPNNNNMLRTNWKISKNAQRIFFBLKPTLRDQNSLPGLVLTCK | 120 | | |
| Dd | 68 | LDENVYTPRTTYQVCQWMEPPNNNNMLRTNWKISKNAQRIFFVEIKPTLRDQNSLPGLVLTCK | 127 | | |
| Qy | 121 | ETFNLYYYETPDYDGRNIRENLYLKIDITIADESFTQGLDERKKKNTLTVREIIGPLSKK | 180 | | |
| Dd | 128 | ETFNLYYYETPDYDGRNIRENLYLKIDITIADESFTQGLDERKKKNTLTVREIIGPLSKK | 187 | | |
| Qy | 181 | GFYLAPODVACIALVSVKYYKKCKWTIVENILAVFPDVTSGSEFSLVEVGTCVSSAAE | 240 | | |
| Dd | 188 | GFYLAPODVACIALVSVKYYKKCKWTIENILAIIPDVTSGSEFSLVEVGTCVSSAAE | 247 | | |
| Qy | 241 | EAEVSPRHHCAGEEMLVPIGKCTCKAQYQKQDTCCECGRRPFYSSSSQDIQCSPCPHHS | 300 | | |

| | | | | | |
|----|-----|--------------------------|---------------------|----------------------|------|
| Db | 248 | EAEINAPRMCHSAGEWLVPIGKCI | CKAGVQOKGDPCECGF | KSSSQDQCRCPTHS | 3078 |
| Qy | 301 | FSPRESSSSCEDEGDGYRAP | SPDPVYACTRPSAPQNI | FININTYTSLEMSPADNGR | 3668 |
| Db | 308 | FSKSESSSSCEDEGDGYRAP | SDPPVYACTRPSAPQNI | FININTYTSLEMSPADNGR | 3678 |
| Qy | 361 | NDVTYRITLCKRCSMEGCEV | PCGSNIGYMPQOTGLBNDY | VYVMDLLAHANTYPEAVNG | 4208 |
| Db | 368 | NDVTYRITLCKRCSMEGCEV | PCGSNIGYMPQOTGLBNDY | VYVMDLLAHANTYPEAVNG | 4218 |
| Qy | 421 | VSLSSSSQRLPAAVSTTTGQAP | PSQVSGVMKERYLQRS | VSLSSMDEPHPNVITEYIKY | 4888 |
| Db | 428 | VSLSSSSQRLPAAVSTTTGQAP | PSQVSGVMKERYLQRS | VSLSSMDEPHPNVITEYIKY | 4898 |
| Qy | 481 | YEDQQRERYSTLTKTSTAS | INNLKPKPTVVYFOIRAT | YAAAGYGNYSBRLDVA | 5408 |
| Db | 488 | YEDQQRERYSTLTKTSTAS | INNLKPKPTVVYFOIRAT | YAAAGYGNYSBRLDVA | 5418 |
| Qy | 541 | KMEEARAVSSQNPPVITIA | VAVAGTITLTFPVRFGI | GRHCGSYRADQGDDELTFH | 5998 |
| Db | 548 | KMEEARAVSSQNPPVITIA | VAVAGTITLTFPVRFGI | GRHCGSYRADQGDDELTFH | 6008 |

RESULT 14
US-08-449-645A-13
; Sequence 13, Application US/08449645A

TITLE OF INVENTION: Eph-Like Receptor Protein Ty
 TITLE OF INVENTION: Kinases
 NUMBER OF SEQUENCES: 43
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Angen Patent Operations/RBW
 STREET: 1840 Dehavilland Road
 CITY: Thousand Oaks
 STATE: California
 COUNTRY: USA
 ZIP: 91320
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.3005
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/449,645A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Winter, Robert B.
 REFERENCE/DOCKET NUMBER: A-287
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 991 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-449-645A-13

[illegible]

```

Db      128 NMITYFSDDDNGNRIKENOYIKIDTIAADSFTELDIGDRVMKLNTEVRDVVPLSKKGFY 187
Qy      184 LAFQDVACIALYVSVKYKKCWITVENLAVFPDVTGSEFSSLVEVRGTCVSSABEEAE 243
Db      188 LAFQDVACIALYVSVRYKKCPVNHVLAVFPDITIGADSSQLLEVSQCVN--HSVTD 245
Qy      244 NSPRMHCASAGEWLVPIGKICAKAGYQOKGDTCEPCGRFRFYKSSQDLQCSRCPTHSFSD 303
Db      246 EPRPMHCASAGEWLVPIGKICAKAGYEENKGTCCVCRPFKASPHIQCSCGPCPHSYTH 305
Qy      304 REGSSRCECEGDYRRASDPPEYVACTRPPSAPONLININQVTSLEWSPADNGGRNDV 363
Db      306 EEAISTCVCCEKDYFRRESDPPTMACTRPSPAPRNALSNVNETSVFLEMTIPADTGGRKDV 365
Qy      364 TYRILCKRCSEWQEGECVPCGSGNIGMPDQGTGLDENVTYVMDLAAHANYTEVEAVNGVSD 423
Db      366 SYIACKCKNSHAGVCECGGHVRYLPQSGLNKNTSVMMVDLANTNYFEIEAVNGVSD 425
Qy      424 LSRQRLFAAVSTTTGQAAPSOVSQVKKERYLQRSVQLSWQEPHNGVITEIKYEEK 483
Db      426 LSPGARQYVSVNVTNOAAPSPVTNVKKGIAKNSISLSWQEPDRPNGIILEYEIKHPEK 485
Qy      484 DORERTYSLTKTSTASINNLKPGTVYVFOIRAVTAAGYGNVSPRLDVATLEBASGMF 543
Db      486 DQ-ETSTTIKSKETTTTAEGLKPAASYVFOIRAKTAAGVFSRRFE-----F 533
Qy      544 EAT---AVSSEQNPVITIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQEGDEE-LYFH 599
Db      534 ETPVPFAASDQSQIPVIAVSVTVG-VILLAVIGVLLSGRCGYSKAKQDPREEKMHFH 592
Qy      600 SLVTNEHLAV 609
Db      593 ----NGHIKL 598

RESULT 15
US-08-702-367A-13
; Sequence 13, Application US/08702367A
; Patent No. 5981246
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; TITLE OF INVENTION: Eph-like Receptor Protein Tyrosine
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Patent Operations/RBW
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702,367A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wincer, Robert B.
; REFERENCE/DOCKET NUMBER: A-287
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 991 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-702-367A-13

```

Query Match 56.8%; Score 1843; DB 2; Length 991;
 Best Local Similarity 56.9%; Pred. No. 7,3e-163;

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Matches 347; Conservative 98; Mismatches 135; Indels 30; Gaps 9;
Qy      6 RPPSW--IILCYITMLGFAHTGEAOAAKEVLLDLSKAOOTELEMISPPSGWBEISGLDE 63
Db      13 RAFLMTCLLC-----AARTLLAPSPNEVNLIDSTVMQDGLGWIAPPKNGWEIEGVIDE 67
Qy      64 NYPIRTTYQCVQMEPRQNNMLFTNWSISGNAORIVELKFTLRDQNSLPVUGTCKETP 123
Db      68 NYAPIHTYQVCKMEQNNMLTSMWISNEGASRIIEIKFTLRDQNSLPGGIGTCKETP 127
Qy      124 NLVYFEDVDGTGNIRENLVVKIDTIAADESPFQGLGERKMKLNTEVEBIGPLSKKGFY 183
Db      128 NMITYFSDDDNGNRIKENOYIKIDTIAADSFTELDIGDRVMKLNTEVRDVVPLSKKGFY 187
Qy      184 LAFQDVACIALYVSVKYKKCWITVENLAVFPDVTGSEFSSLVEVRGTCVSSABEEAE 243
Db      188 LAFQDVACIALYVSVRYKKCPVNHVLAVFPDITIGADSSQLLEVSQCVN--HSVTD 245
Qy      244 NSPRMHCASAGEWLVPIGKICAKAGYQOKGDTCEPCGRFRFYKSSQDLQCSRCPTHSFSD 303
Db      246 EPRPMHCASAGEWLVPIGKICAKAGYEENKGTCCVCRPFKASPHIQCSCGPCPHSYTH 305
Qy      304 REGSSRCECEGDYRRASDPPEYVACTRPPSAPONLININQVTSLEWSPADNGGRNDV 363
Db      306 EEAISTCVCCEKDYFRRESDPPTMACTRPSPAPRNALSNVNETSVFLEMTIPADTGGRKDV 365
Qy      364 TYRILCKRCSEWQEGECVPCGSGNIGMPDQGTGLDENVTYVMDLAAHANYTEVEAVNGVSD 423
Db      366 SYIACKCKNSHAGVCECGGHVRYLPQSGLNKNTSVMMVDLANTNYFEIEAVNGVSD 425
Qy      424 LSRQRLFAAVSTTTGQAAPSOVSQVKKERYLQRSVQLSWQEPHNGVITEIKYEEK 483
Db      426 LSPGARQYVSVNVTNOAAPSPVTNVKKGIAKNSISLSWQEPDRPNGIILEYEIKHPEK 485
Qy      484 DORERTYSLTKTSTASINNLKPGTVYVFOIRAVTAAGYGNVSPRLDVATLEBASGMF 543
Db      486 DQ-ETSTTIKSKETTTTAEGLKPAASYVFOIRAKTAAGVFSRRFE-----F 533
Qy      544 EAT---AVSSEQNPVITIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQEGDEE-LYFH 599
Db      534 ETPVPFAASDQSQIPVIAVSVTVG-VILLAVIGVLLSGRCGYSKAKQDPREEKMHFH 592
Qy      600 SLVTNEHLAV 609
Db      593 ----NGHIKL 598

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Search completed: August 23, 2005, 08:27:34
 Job time : 23.2217 secs

XX Example 1; Page 109-111; 128pp; English.

CC cDNA cloning using adult mouse brains and Northern blotting identified 2
CC truncated versions, MDK1 T1 (AAW03422) and MDK1 T2 (AAW03423), of the
CC novel mouse developmental kinase 1 (MDK1) (see also AAW03421), a new
CC member of the eck/eph family of receptor tyrosine kinases. Their amino
CC acid sequences were deduced from cDNA clones (AA132961 and AA132962)
CC obtd. from adult mouse brains. MDK T1 and T2 each possesses the entire
CC ectodomain, the transmembrane domain and part of the juxtamembrane region
CC of MDK1, but lack the catalytic tyrosine kinase domain. They can be used
CC to screen for potential agents useful for treatment of diseases
CC characterised by abnormal signal transduction
CC
XX

Sequence 610 AA;

Query Match 100.0%; Score 3243; DB 2; Length 610;
Best Local Similarity 100.0%; Pred. No. 2.3e-275;
Matches 610; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTQTRPSPSWIIICYYLWLGFAHTGEAQAKEVLLDLSKAQOTLEWISSPPSGMERISG 60
DB 1 MVTQTRPSPSWIIICYYLWLGFAHTGEAQAKEVLLDLSKAQOTLEWISSPPSGMERISG 60
QY 61 LDENYTPIRITYQVCQWEPNQNMLRTNWSKNAORIFVELKFTLRDCKSLPGVLTGCK 120
DB 61 LDENYTPIRITYQVCQWEPNQNMLRTNWSKNAORIFVELKFTLRDCKSLPGVLTGCK 120
QY 121 ETEFNLYYYETDYGGRNIRENLVYKIDTIAADESFTQGDIGERRMKLNTVREIGPLSKK 180
DB 121 ETEFNLYYYETDYGGRNIRENLVYKIDTIAADESFTQGDIGERRMKLNTVREIGPLSKK 180
QY 181 GFYLAPODVACIALVSVKYYKKCWTIVENLAVFPDVTGSEFSSSLVEVRGTCVSSAEE 240
DB 181 GFYLAPODVACIALVSVKYYKKCWTIVENLAVFPDVTGSEFSSSLVEVRGTCVSSAEE 240
QY 241 EAENSPPMHCSABGEMLVPIGKCI CKAGYQOKGDTCEPCGRFRPKSSSOLQSRCTHS 300
DB 241 EAENSPPMHCSABGEMLVPIGKCI CKAGYQOKGDTCEPCGRFRPKSSSOLQSRCTHS 300
QY 301 FSRREGSSRCCEGEGYRAPSDPPYACTRPPSAPOULININQTTVSLFMSPPADNGGR 360
DB 301 FSRREGSSRCCEGEGYRAPSDPPYACTRPPSAPOULININQTTVSLFMSPPADNGGR 360
QY 361 NDVTYRILCKRCSEWQEGECVPCGSGNIGYMPQGTLEEDNYVTVMDLAAHAYTEVEAVNG 420
DB 361 NDVTYRILCKRCSEWQEGECVPCGSGNIGYMPQGTLEEDNYVTVMDLAAHAYTEVEAVNG 420
QY 421 VSDLSRQRLFAVASTTTGQAAPSQVSGWKERYLQRSVOLSMOEPHPHGVITTEYIKY 480
DB 421 VSDLSRQRLFAVASTTTGQAAPSQVSGWKERYLQRSVOLSMOEPHPHGVITTEYIKY 480
QY 481 YEKDQRRRTYSTLTKSTASINNLLKPGTYVPOIRVTAAGYGNVSPRIDVATLEBASG 540
DB 481 YEKDQRRRTYSTLTKSTASINNLLKPGTYVPOIRVTAAGYGNVSPRIDVATLEBASG 540
QY 541 KMEEATAVSSEONVILIAVAVAGTIIIVFMVGFIIIGRRHCGYSKADLEGDEELYFHS 600
DB 541 KMEEATAVSSEONVILIAVAVAGTIIIVFMVGFIIIGRRHCGYSKADLEGDEELYFHS 600
QY 601 LVTNEHLSTL 610
DB 601 LVTNEHLSTL 610

RESULT 2

ID AAW03423 standard; protein; 626 AA.

XX AAW03423;

XX 11-NOV-1996 (first entry)

DE Mouse developmental kinase 1 MDK1 T2.

KM Mouse developmental kinase 1; MDK1 T2; receptor tyrosine kinase; RTK;
KW signal transduction; probe; diagnosis; gene therapy; neurodegeneration;
KW neuroproliferation; cancer.

XX Mus sp.

OS

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/note="product of alternative splicing"

PN WC9621013-A1.

PD 11-JUL-1996.

PF 03-JAN-1996; 96MO-US000419.

PR 03-JAN-1995; 95US-00368776.

PA (SUGR-) SUGEN INC.

PI (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

PI Closek T, Ullrich A, Millaer B;

PI WPI; 1996-333988/33.

DR N-PSDB; AA132962.

PT New mouse development kinase 1 gene - used for developing prods. for

PS diagnosis and treatment of abnormalities in signal transduction pathways.

PS Example 1; Page 113-115; 128pp; English.

CC cDNA cloning using adult mouse brains and Northern blotting identified 2

CC truncated versions, MDK1 T1 (AAW03422) and MDK1 T2 (AAW03423), of the

CC novel mouse developmental kinase 1 (MDK1) (see also AAW03421), a new

CC member of the eck/eph family of receptor tyrosine kinases. Their amino

CC acid sequences were deduced from cDNA clones (AA132961 and AA132962)

CC obtd. from adult mouse brains. MDK T1 and T2 each possesses the entire

CC ectodomain, the transmembrane domain and part of the juxtamembrane region

CC of MDK1, but lack the catalytic tyrosine kinase domain. They can be used

CC to screen for potential agents useful for treatment of diseases

CC characterised by abnormal signal transduction

CC
XX

Sequence 626 AA;

Query Match 98.6%; Score 3199; DB 2; Length 626;

Best Local Similarity 100.0%; Pred. No. 1.7e-271;
Matches 601; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVTQTRPSPSWIIICYYLWLGFAHTGEAQAKEVLLDLSKAQOTLEWISSPPSGMERISG 60
DB 1 MVTQTRPSPSWIIICYYLWLGFAHTGEAQAKEVLLDLSKAQOTLEWISSPPSGMERISG 60
QY 61 LDENYTPIRITYQVCQWEPNQNMLRTNWSKNAORIFVELKFTLRDCKSLPGVLTGCK 120
DB 61 LDENYTPIRITYQVCQWEPNQNMLRTNWSKNAORIFVELKFTLRDCKSLPGVLTGCK 120
QY 121 ETEFNLYYYETDYGGRNIRENLVYKIDTIAADESFTQGDIGERRMKLNTVREIGPLSKK 180
DB 121 ETEFNLYYYETDYGGRNIRENLVYKIDTIAADESFTQGDIGERRMKLNTVREIGPLSKK 180
QY 181 GFYLAPODVACIALVSVKYYKKCWTIVENLAVFPDVTGSEFSSSLVEVRGTCVSSAEE 240

Db 181 GFYLAPODVAGACIALVSKYKKWTIVENLAVFPDVTGSEFSSSLVEVRGTCVSSAEE 240
Qy 241 EAENSPPMHCSAEGEMLVPIGKCI CKAGYQOKGPTCEPCGRRFYKSSSODLQCSRCPH 300
Db 241 EAENSPPMHCSAEGEMLVPIGKCI CKAGYQOKGPTCEPCGRRFYKSSSODLQCSRCPH 300
Qy 301 FSDREGSSRCCEDEGYRAPSDPPYVACTRPPAPQULFININOTTVLSLEMSPPADNGR 360
Db 301 FSDREGSSRCCEDEGYRAPSDPPYVACTRPPAPQULFININOTTVLSLEMSPPADNGR 360
Qy 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQOTGLEBNYTVMDLLAHANTTFEVAVNG 420
Db 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQOTGLEBNYTVMDLLAHANTTFEVAVNG 420
Qy 421 VSDLSRSQRLFAAVSITTTGAAPSOVGVKMERVLQSRVLSQWEPHPNGVITEYEIKY 480
Db 421 VSDLSRSQRLFAAVSITTTGAAPSOVGVKMERVLQSRVLSQWEPHPNGVITEYEIKY 480
Qy 481 YEKDQERTYSTLTKTSTASINNLKPGTVVFPQIRAVTAAGYGNYSRPLDVALTEBASG 540
Db 481 YEKDQERTYSTLTKTSTASINNLKPGTVVFPQIRAVTAAGYGNYSRPLDVALTEBASG 540
Qy 541 KMEFATVSSSEONPVIIIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQEGDELYFHS 600
Db 541 KMEFATVSSSEONPVIIIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQEGDELYFHS 600
Qy 601 L 601
Db 601 L 601

RESULT 3

ID AAM03421 standard; protein; 998 AA.
XX AAM03421;
XX 11-NOV-1996 (first entry)
XX
XX Mouse developmental kinase 1.
XX
XX Mouse developmental kinase 1; MDK1; receptor tyrosine kinase; RTK;
XX signal transduction; probe; diagnosis; therapy; neurodegeneration;
XX neuroproliferation; cancer.
XX Mus sp.
XX
XX Key Location/Qualifiers
XX Peptide 1..28
XX Modified-site /label= sig_peptide
XX Modified-site 64..66
XX Modified-site /label= N-glycosylation_site
XX Modified-site 343..345
XX Modified-site /label= N-glycosylation_site
XX Modified-site 410..412
XX Domain /label= N-glycosylation_site
XX 555..579
XX /label= Transmembrane_domain
XX
XX WO9621013-A1.
XX
XX 11-JUL-1996.
XX
XX 03-JAN-1996. 96WO-US000419.
XX
XX 03-JAN-1995; 95US-00368776.
XX
XX (SUGC-) SUGEN INC.
XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
XX Clobesek T, Ulrich A, Millauer B;
XX

DR WPI; 1996-333988/33.
DR N-PSDB; AAT32960.
XX
XX New mouse development kinase 1 gene - used for developing prods. for
XX diagnosis and treatment of abnormalities in signal transduction pathways.
XX
XX Example 1; Page 105-108; 128pp; English.
XX
XX Mouse developmental kinase 1 (MDK1) (AAM03421) is a new member of the
XX eck/eph family of receptor tyrosine kinases (RTKs). Its amino acid
XX sequence was deduced from a cDNA clone (AAT32960) isolated from mouse
XX embryo and adult brain libraries. The distinct patterns of MDK1
XX expression during mouse development suggest an important role for MDK1 in
XX the formation of neuronal structures. MDK1 may be obt'd. by expression in
XX host cells. It can be used in methods for the diagnosis of diseases
XX characterised by abnormality in a signal transduction pathway, such as
XX neuroproliferative or neurodegenerative disorders or cancer, to screen
XX for (ant)agonists, and to raise antibodies

Sequence 998 AA;

Query Match 98.4%; Score 3191; DB 2; Length 998;
Best Local Similarity 100.0%; Pred. No. 1,8e-270; Indels 0; Gaps 0;
Matches 599; Conservative 0; Mismatches 0;

Qy 1 MVVQTRPSPWIIICYLWLGFAHTGEAQAKEYLLDLSKAQTELEWISSPPSGMEISG 60
Db 1 MVVQTRPSPWIIICYLWLGFAHTGEAQAKEYLLDLSKAQTELEWISSPPSGMEISG 60
Qy 61 LDENYTPIRTYQVCQWEPNQNNMLRTNWSKGNACRI FVELKFTLLDNCNSLPGVLCCK 120
Db 61 LDENYTPIRTYQVCQWEPNQNNMLRTNWSKGNACRI FVELKFTLLDNCNSLPGVLCCK 120
Qy 121 ETEFLYYETDVTGRIRENLYVKIDTIADESFTQDGERRMKNTREIRGPIKSK 180
Db 121 ETEFLYYETDVTGRIRENLYVKIDTIADESFTQDGERRMKNTREIRGPIKSK 180
Qy 181 GFYLAPODVAGACIALVSKYKKWTIVENLAVFPDVTGSEFSSSLVEVRGTCVSSAEE 240
Db 181 GFYLAPODVAGACIALVSKYKKWTIVENLAVFPDVTGSEFSSSLVEVRGTCVSSAEE 240
Qy 241 EAENSPPMHCSAEGEMLVPIGKCI CKAGYQOKGPTCEPCGRRFYKSSSODLQCSRCPH 300
Db 241 EAENSPPMHCSAEGEMLVPIGKCI CKAGYQOKGPTCEPCGRRFYKSSSODLQCSRCPH 300
Qy 301 FSDREGSSRCCEDEGYRAPSDPPYVACTRPPAPQULFININOTTVLSLEMSPPADNGR 360
Db 301 FSDREGSSRCCEDEGYRAPSDPPYVACTRPPAPQULFININOTTVLSLEMSPPADNGR 360
Qy 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQOTGLEBNYTVMDLLAHANTTFEVAVNG 420
Db 361 NDVTYRILCKRCSEWEGECVPCGSNIGYMPQOTGLEBNYTVMDLLAHANTTFEVAVNG 420
Qy 421 VSDLSRSQRLFAAVSITTTGAAPSOVGVKMERVLQSRVLSQWEPHPNGVITEYEIKY 480
Db 421 VSDLSRSQRLFAAVSITTTGAAPSOVGVKMERVLQSRVLSQWEPHPNGVITEYEIKY 480
Qy 481 YEKDQERTYSTLTKTSTASINNLKPGTVVFPQIRAVTAAGYGNYSRPLDVALTEBASG 540
Db 481 YEKDQERTYSTLTKTSTASINNLKPGTVVFPQIRAVTAAGYGNYSRPLDVALTEBASG 540
Qy 541 KMEFATVSSSEONPVIIIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQEGDELYFHS 599
Db 541 KMEFATVSSSEONPVIIIAVAVAGTIIIVFMVFGFIIGRRHCGYSKADQEGDELYFHS 599

RESULT 4

ID ADM87167 standard; protein; 945 AA.
XX ADM87167;
XX
XX 03-JUN-2004 (first entry)
XX

XX Human protein SEQ ID NO:260.
DE
XX
XX respiratory; cytosolic; antiarthritic; antiinflammatory;
KM gastrointestinal; antibacterial; immunosuppressive; antidiabetic;
KM antineutritic; gene therapy; molecular weight marker; chromosome marker;
KM chromosome tag; genetic fingerprinting; nutritional supplement; cancer;
KM inflammatory condition; arthritis; inflammatory bowel disease;
KM Crohn's disease; sepsis; rheumatoid arthritis; diabetes mellitus type 1;
KM graft versus host disease; human.
XX
XX Homo sapiens.
OS
XX WO2004009834-A2.
PN
XX 29-JAN-2004.
PD
XX 19-JUL-2002; 2002MO-US022858.
PF
XX 21-JUL-2001; 2001US-0306971P.
PR 28-MAR-2002; 2002US-00112944.
XX
XX (NUVE-) NUVELO INC.
PA
XX Tang YT, Yang Y, Weng G, Zhang J, Ren F, Xue A, Wang J;
PI Wehrman T, Ghosh MJ, Wang D, Zhao QA, Wang Z;
XX WPI; 2004-143291/14.
DR N-PSDB; ADM66923.
XX
XX New isolated polynucleotides and polypeptides, useful for treating, e.g.
PT cancer, lung or liver fibrosis, arthritis, inflammatory bowel disease,
PT Crohn's disease, rheumatoid arthritis, diabetes mellitus type 1 or graft
PT versus host disease.
XX
XX Claim 20; SEQ ID NO 260; 591pp; English.
PS
XX The present invention describes an isolated polynucleotide (I): (a)
CC comprising a nucleotide sequence selected from SEQ ID NO:1-244; or (b)
CC which encodes a polypeptide with biological activity, where the
CC polynucleotide hybridises to (I) under stringent hybridisation conditions
CC or has greater than 98% sequence identity with (I). (I) has respiratory,
CC cytosolic, antiarthritic, antiinflammatory, gastrointestinal,
CC antibacterial, immunosuppressive, antidiabetic and antineutritic
CC activities, and can be used in gene therapy. (I) can be used for
CC generating polynucleotides encoding chimeric or fusion proteins and
CC heterologous protein sequences. The polynucleotides can be used to
CC express recombinant protein for analysis, characterisation or therapeutic
CC use; as markers for tissues in which the corresponding protein is
CC preferentially expressed; as molecular weight markers on gels; as
CC chromosome markers or tags to identify chromosomes or to map related gene
CC positions; to compare with endogenous DNA sequences in patients to
CC identify potential genetic disorders; as probes to hybridise and discover
CC genes, related DNA sequences; as a source of information to derive PCR
CC primers for genetic fingerprinting; as a probe to substract-out known
CC sequences in the process of discovering other novel polynucleotides; for
CC selecting and making oligomers for attachment to a gene chip or other
CC support, including for examination of expression patterns; to raise anti-
CC protein antibodies using DNA immunisation techniques; and as an antigen
CC to raise anti-DNA antibodies or elicit another immune response. The
CC polynucleotides and polypeptides can also be used as nutritional sources
CC or supplements, e.g. as a protein or amino acid supplement, as a carbon
CC source, as a nitrogen source or as a source of carbohydrates. The
CC polynucleotides and polypeptides can also be used treat cancer. The
CC compositions are useful for promoting better or faster closure of non-
CC healing wounds, for the generation and regeneration of tissues, for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues, and conditions resulting from
CC systemic cytokine damage. The compositions can also be used to treat
CC inflammatory conditions (e.g. arthritis, inflammatory bowel disease or
CC Crohn's disease), sepsis, rheumatoid arthritis, diabetes mellitus type 1
CC or graft versus host disease. The present sequence represents a novel
CC human polypeptide sequence from the present invention. N.B. The sequences

CC for this patent were obtained from the USPTO web site from an equivalent
CC US patent US20040048249A1.
XX
XX
SQ Sequence 945 AA;
Query Match 96.8%; Score 3139; DB 8; Length 945;
Best Local Similarity 97.7%; Pred. No. 6, 2e-266;
Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0;
QY 1 MVTQTFPSPWIIICYYIMLGFATHTGEAQAKEYLLDLSAQOQTELEWISSPPSGWEEISG 60
DB 1 MVTQTFPSPWIIICYYIMLGFATHTGEAQAKEYLLDLSAQOQTELEWISSPPSGWEEISG 60
QY 1DENYTPIRTYQVCQWMEPNQNNMLFTNWSKNAQRIFVELKFTLRDCNSLPGLGTCK 120
DB 61 1DENYTPIRTYQVCQWMEPNQNNMLFTNWSKNAQRIFVELKFTLRDCNSLPGLGTCK 120
QY 121 EFNFLYYEFTDVTGNTIRENLVYKIDTIAADESFTQSGDLGERKMLNTEVREISGLSKK 180
DB 121 EFNFLYYEFTDVTGNTIRENLVYKIDTIAADESFTQSGDLGERKMLNTEVREISGLSKK 180
QY 181 GFYLAFOVQACIALYSVKYKCKWTIVENLAVFPDVTGSEFSSLVEVRGTCVSAER 240
DB 181 GFYLAFOVQACIALYSVKYKCKWTIVENLAVFPDVTGSEFSSLVEVRGTCVSAER 240
QY 241 EANSBPMHCSABGEMLVPIGKCICRAGYQOKGDTCEPCGRPFYKSSODLQCSRCPYHS 300
DB 241 EANSBPMHCSABGEMLVPIGKCICRAGYQOKGDTCEPCGRPFYKSSODLQCSRCPYHS 300
QY 301 FSDRESSSRCEGCDGYRAPSDPPYACRPPAPQNLFINOTVLSLEWSPDANGR 360
DB 301 FSDRESSSRCEGCDGYRAPSDPPYACRPPAPQNLFINOTVLSLEWSPDANGR 360
QY 361 NDVTYRILCKRCSEWEGECVPCGSNIGWMPQGTGLBDNVTYVMDLHANYTEVAUNG 420
DB 361 NDVTYRILCKRCSEWEGECVPCGSNIGWMPQGTGLBDNVTYVMDLHANYTEVAUNG 420
QY 421 VSDLSRSQRIFAVSIITGQAPBSQVGVKKEKRVQLSQWEPENHNGVITEYIKY 480
DB 421 VSDLSRSQRIFAVSIITGQAPBSQVGVKKEKRVQLSQWEPENHNGVITEYIKY 480
QY 481 YEKQGERYTSILKTKSTASINNLKRGTYVYQIRAVYAAAGGNSPRLDVATLEASG 540
DB 481 YEKQGERYTSILKTKSTASINNLKRGTYVYQIRAVYAAAGGNSPRLDVATLEASG 540
QY 541 KMFEATAVSSEQNPIIIVAVAGTIIIVFWFGFIIGRRHCGYSKADQEGDELYFH 599
DB 541 KMFEATAVSSEQNPIIIVAVAGTIIIVFWFGFIIGRRHCGYSKADQEGDELYFH 599
RESULT 5
AAR85092
ID AAR85092 standard; protein; 998 AA.
XX
AC AAR85092;
XX
XX 16-APR-1996 (first entry)
DT
XX
DE EPH-like receptor protein tyrosine kinase HEK11.
XX
KM EPH-like receptor protein tyrosine kinase; PK; HEK11;
KW human eph-like kinase; therapy; diagnosis; antibody; vector.
XX
OS Homo sapiens.
XX
PN WO9528484-A1.
XX
XX 26-OCT-1995.
PD
XX 14-APR-1995; 95MO-US004681.
PF
XX 15-APR-1994; 94US-00229509.
PR
XX

PA (AMGE-) AMGEN INC.
 XX Fox GM, Welcher AA, Jing S;
 XX WPI: 1995-373799/48.
 DR N-PSDB; AAT02949.
 XX
 XX New nucleic acid encoding EPH-like receptor tyrosine kinase(s) - and
 PT related vectors, host cells, proteins, antibodies etc., used
 PT diagnostically and therapeutically to modulate receptor activation or
 PT prodn.
 PS
 PS Claim 18; Page 71-75; 133pp; English.
 XX
 XX 4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7,
 CC HEK8 and HEK11 (AAR85089-92), respectively, were identified following
 CC isolation of their encoding cDNAs (AAT02946-49) from a human foetal brain
 CC cDNA library. HEK5, HEK7 and HEK8 show extensive homology to the
 CC catalytic domain of chicken EPH-like receptors Cek5, Cek7 and Cek8. HEK11
 CC shows no homology to any known EPH-like receptor. Recombinant HEK
 CC receptors (or their soluble extracellular domains) are produced by
 CC expression of encoding sequences in prokaryotic or eucaryotic host cells,
 CC and are used to produce antibodies (utilised in diagnostic assays), or to
 CC identify and purify ligands for HEK receptors, or therapeutically to
 CC modulate the activation of cell-associated receptors
 CC
 XX Sequence 998 AA;
 XX
 Query Match 96.8%; Score 3139; DB 2; Length 998;
 Best Local Similarity 97.7%; Pred. No. 6.8e-266;
 Matches 585; Conservative 10; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MVVOTRPPSWIIICYIMLGFATGEOAQAKEYLLDSKAQOETELWISSPPGMEIISG 60
 DB 1 MVTOTRPPSWIIICYIMLGFATGEOAQAKEYLLDSKAQOETELWISSPPGMEIISG 60
 QY 61 LDENVYTRIRTYOVQVMEPNQNNMLRTNWSKNAQRIFVELKFTLRDQNSLPVLTGTC 120
 DB 61 LDENVYTRIRTYOVQVMEPNQNNMLRTNWSKNAQRIFVELKFTLRDQNSLPVLTGTC 120
 QY 121 ETPFLYYEYDYGGRNIRENLVYKIDTIADESFTQDGLGERKMKLNTVREIGPLSKK 180
 DB 121 ETPFLYYEYDYGGRNIRENLVYKIDTIADESFTQDGLGERKMKLNTVREIGPLSKK 180
 QY 181 GFYLAPODVGACIALVSKYKVKCMTIVENLAFPPDVNVSSEFSSSLVEVNGTCVSSAEE 240
 DB 181 GFYLAPODVGACIALVSKYKVKCMTIVENLAFPPDVNVSSEFSSSLVEVNGTCVSSAEE 240
 QY 241 EAENSPPMHCSAEGEWLVPIGKCIKAGYQOKGDTCEFCGRFFYKSSSODLQCSRPTHS 300
 DB 241 EAENSPPMHCSAEGEWLVPIGKCIKAGYQOKGDTCEFCGRFFYKSSSODLQCSRPTHS 300
 QY 301 FSDREGSSRCCEGYYRAPSDPRVACTRPPSAPNLIINOTVYSLWSPPADNGCR 360
 DB 301 FSDREGSSRCCEGYYRAPSDPRVACTRPPSAPNLIINOTVYSLWSPPADNGCR 360
 QY 361 NDVYTRILCKRCSMEQECVCGSNIGMPQQTGLEDYVVMMLLAHANTFEVAVNG 420
 DB 361 NDVYTRILCKRCSMEQECVCGSNIGMPQQTGLEDYVVMMLLAHANTFEVAVNG 420
 QY 421 VSDLSRSQRLFAAVSITTGQAPSOVSQVMEKERVLOBSVOLSMQEPHNGVITEYEIKY 480
 DB 421 VSDLSRSQRLFAAVSITTGQAPSOVSQVMEKERVLOBSVOLSMQEPHNGVITEYEIKY 480
 QY 481 YEKQQRERTYSTLTSTKSTASINNLKPGTVVFOIRAVTAAGYNNYSPRLDVATLEASG 540
 DB 481 YEKQQRERTYSTLTSTKSTASINNLKPGTVVFOIRAVTAAGYNNYSPRLDVATLEASG 540
 QY 541 KMFEPATVSSSQNVIIIAVAVAGTIIIVMVGFIIGRRHGYSSADODGDELEIFH 599
 DB 541 KMFEPATVSSSQNVIIIAVAVAGTIIIVMVGFIIGRRHGYSSADODGDELEIFH 599

RESULT 6
 AAR85090
 ID AAR85090 standard; protein; 991 AA.
 XX
 XX AAR85090;
 AC
 AC 16-APR-1996 (first entry)
 DT
 DT EPH-like receptor protein tyrosine kinase HEK7.
 DE
 DE EPH-like receptor protein tyrosine kinase; PTG; HEK7;
 KM human eph-like kinase; therapy; diagnosis; vector; antibody.
 KM
 KM Homo sapiens.
 OS
 OS MO9528484-A1.
 PN
 PN 26-OCT-1995.
 PD
 PD 14-APR-1995; 95WO-US004681.
 PF
 PF 15-APR-1994; 94US-00229509.
 PR
 PR (AMGE-) AMGEN INC.
 PA
 PA Fox GM, Welcher AA, Jing S;
 PI WPI: 1995-373799/48.
 PI N-PSDB; AAT02947.
 DR
 DR New nucleic acid encoding EPH-like receptor tyrosine kinase(s) - and
 PT related vectors, host cells, proteins, antibodies etc., used
 PT diagnostically and therapeutically to modulate receptor activation or
 PT prodn.
 PT
 PS
 PS Claim 18; Page 54-57; 133pp; English.
 PS
 PS 4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7,
 CC HEK8 and HEK11 (AAR85089-92), respectively, were identified following
 CC isolation of their encoding cDNAs (AAT02946-49) from a human foetal brain
 CC cDNA library. HEK5, HEK7 and HEK8 show extensive homology to the
 CC catalytic domain of chicken EPH-like receptors Cek5, Cek7 and Cek8. HEK11
 CC shows no homology to any known EPH-like receptor. Recombinant HEK
 CC receptors (or their soluble extracellular domains) are produced by
 CC expression of encoding sequences in prokaryotic or eucaryotic host cells,
 CC and are used to produce antibodies (utilised in diagnostic assays), or to
 CC identify and purify ligands for HEK receptors, or therapeutically to
 CC modulate the activation of cell-associated receptors. Soluble HEK7
 CC receptor may primarily affect proliferation and/or differentiation of
 CC brain cells. pancreatic cells
 CC
 XX Sequence 991 AA;
 XX
 Query Match 56.8%; Score 1843; DB 2; Length 991;
 Best Local Similarity 56.9%; Pred. No. 4.9e-152;
 Matches 347; Conservative 98; Mismatches 135; Indels 30; Gaps 9;
 QY 6 RFPWM--IICYIMLGFATGEOAQAKEYLLDSKAQOETELWISSPPGMEIISG 63
 DB 13 RAPLMTCLLIC-----AALRTLLASPSNEVNLDSRTVMDDLGIAPPKGMEIIGEVDE 67
 QY 64 NYTPIRTYOVQVMEPNQNNMLRTNWSKNAQRIFVELKFTLRDQNSLPVLTGTCETP 123
 DB 68 NYAPIRTYOVQVMEPNQNNMLRTNWSKNAQRIFVELKFTLRDQNSLPVLTGTCETP 127
 QY 124 NLYYETDYGGRNIRENLVYKIDTIADESFTQDGLGERKMKLNTVREIGPLSKKGFY 183
 DB 128 NMYEFESDDQNGRNIKENYKIDTIADESFTQDGLGERKMKLNTVREIGPLSKKGFY 187
 QY 184 LAFODVACIALVSKYKVKCMTIVENLAFPPDVNVSSEFSSSLVEVNGTCVSSAEEAE 243
 DB 188 LAFODVACIALVSKYKVKCMTIVENLAFPPDVNVSSEFSSSLVEVNGTCVSSAEEAE 245

KM neurotrophin activity; trkB; proto-oncogene; tyrosine kinase receptor;
 KM binding protein; BDNF; NT-3; diagnosis.
 OS Rattus sp.
 XX US5843749-A.
 XX
 XX
 PD 01-DEC-1998.
 XX
 PF 06-JUN-1995; 95US-00469537.
 XX
 PR 26-JUL-1991; 91US-00736559.
 PR 28-OCT-1993; 93US-00149492.
 PR 17-MAR-1995; 95US-00406247.
 XX
 PA (REG-) REGENERON PHARM INC.
 XX
 PT Maslakowski P, Yancopoulos GD, Maisompierre PC;
 XX WPI; 1999-044584/04.
 DR N-PSDB; AAV70207.
 XX
 PT DNA encoding receptor tyrosine kinase proteins - and corresponding
 PT proteins.
 XX
 PS Example; Fig 22; 194pp; English.
 XX
 CC The present invention describes nucleic acid molecules for *ror-1*, *ror-2*,
 CC *ehk-1* and *ehk-2*. Also described are the corresponding proteins: *Ror-1*,
 CC *Ror-2*, *Ehk-1*, and *Ehk-2*. The proteins are orphan receptor tyrosine
 CC kinases. The present sequence represents rat *Ehk-1*.
 XX
 XX Sequence 1005 AA;
 SQ
 Query Match 56.2%; Score 1824; DB 2; Length 1005;
 Best Local Similarity 54.8%; Pred. No. 2.3e-150;
 Matches 351; Conservative 96; Mismatches 138; Indels 56; Gaps 11;
 6 RFPSEWILCY-----IM-----LLGFAHTGEAQAQAKVLLDSKAQOTLEWISSPPSG 54
 25 RVPASLGLGCTISAPLKGPMWTLCLCALRTLLASPSNEVNLDSRTVLDGMIAPPKNG 84
 55 WEBSIGLDENYPTIRTYQVCVMBPNONNMLRTWISKNAQRIFEVLEKPTLDCNSLPG 114
 85 WEBSIGEDVENYAPLHTYQVCVMEQONNMLTSMISMEGASRFIELEKPTLRDCNSLPG 144
 115 VLGTCKETFNLYETDYGGRNIRENLYKIDITIAADESFTQDGLGERKKMLTEVREI 174
 145 GLGTCKETFNMYEESDDENGRNIRENLYKIDITIAADESFTQDGLGERKKMLTEVREI 204
 175 GLPSKGFYLAFOVVGACIALVSVKYVKKCWITVENLAVPDPTVTSSEPSLVEVGTG 234
 205 GPLSKGFYLAFOVVGACIALVSVKYVKKCPVVRHLAVPDTITGADSSQLLEVGSGC 264
 235 VSSAEEBAENSPPRMHCAEGEMLVPIGKICAKAGYQKGDCEFCGRFRFYKSSQDQCS 294
 265 VN--HSTVDDPDKHCAEGEMLVPIGKICAKAGYQKGDCEFCGRFRFYKSSQDQCS 322
 295 RCPHSGSDREBSRCECEGYYAPSDPPYVACTRPPSPADNLIININOTVSLWSP 354
 323 KCPHSGYTHESASTSCVCEKDYFRRESPPPTMACTRPPSPARNAISVNETSVLEWIP 382
 355 ADNGGRNDVTYRLICRKGCSWEGECVPCGSGNIGMPOOTGEDYVYVMDLAHANYTEE 414
 383 ADTGCGKDVSYTILCKKCNSHAGVCEGCHVRLPQDGLKNTSVMDADLAHNTYTFE 442
 415 VEAANGVSDLSRSQRLPAFVAVSITGQAAPSQVSGVMKERVYQSRVQSLWQEPHPNGVIT 474
 443 IEAANGVSDLSRPGROYVAVVITNQAAPSPVTNVKKGKIAKNSISLSWQEPDPRNGIIL 502
 475 EYEIKYIEKQOREHTYTLTKTSASINNLKPGTVYVFOIRAVTAAGYNGYSPRLDVAT 534
 503 EYEIKYIEKQO-ETSYTIISKETTTIAEGIKPASYVVFQIRARTAGYGVFSRRFE-- 558

QY 535 LEEASGMPEATAV---SSEONPVIILAVAVAGTILVEMVREGFII-----GRR- 581
 DB 559 -----FETTPVFGASNNQSQPIIGVSVTVGVILLAWMI-GFLSSGCECGCGRAS 609
 QY 582 -----HCGSKADQEGDEE-LYFHSLVTNHLSV 609
 DB 610 SLCAVAHPSLIWRGYSKAKQDPEEEKMHPH-----NGHIXL 646
 RESULT 9
 ABR44241.
 ID ABR44241 standard; protein; 1037 AA.
 AC ABR44241;
 XX
 XX
 DT 18-AUG-2003 (first entry)
 XX
 XX Tyrosine kinase EHK-1.
 DE
 XX CD81; neuron; neural degeneration; astrocyte; Nr51; cytosolic; EHK-1;
 KM neuroprotective; nootropic; antiparkinsonian; anticonvulsant; human;
 KM cerebroprotective; gene therapy; tyrosine kinase.
 XX
 XX Homo sapiens.
 OS
 PN WO2003040333-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 07-NOV-2002; 2002WO-US035588.
 XX
 PR 07-NOV-2001; 2001US-0344712P.
 XX
 PA (YESH) UNIV YESHIYA EINSTEIN COLLEGE.
 PI Weinstein DE, Suarez C, Zerlin M;
 XX WPI; 2003-441557/41.
 DR N-PSDB; ACC78163.
 XX
 PT Enhancing survival of neurons, useful for treating neural degeneration
 PT (e.g. Alzheimer's disease) or a defect in astrocyte proliferation (e.g.
 PT astrocytosis), comprises contacting the neurons with CD81 protein or its
 PT derivative.
 XX
 PS Claim 29; Fig 28; 59pp; English.
 XX
 CC The invention relates to enhancing survival of neurons and involves
 CC contacting the neurons with CD81 protein or CD81 derivative, or its
 CC stabilized variants, in an amount that enhances survival of the neurons.
 CC The method is useful for treating neural degeneration or a condition
 CC associated with a defect in astrocyte proliferation in a mammal, and
 CC involves activating Nr51 or CD81 in the mammal. The method is useful in
 CC treating neural degeneration (e.g. Alzheimer's disease, amyotrophic
 CC lateral sclerosis, Binswanger's disease, Huntington's chorea, multiple
 CC sclerosis, myasthenia gravis, Parkinson's disease, Pick's disease,
 CC cerebral palsy, congenital hydrocephalus, muscular dystrophy, stroke or
 CC vascular dementia) or a condition associated with a defect in astrocyte
 CC proliferation, such as astrocytosis or astrocytoma. The present sequence
 CC represents a the EHK-1 protein (the Nr51 protein has been previously
 CC identified as an orphan receptor tyrosine kinase termed EHK-1 -GenBank
 CC Accession No. XM_046083.2.)
 CC
 XX
 SQ Sequence 1037 AA;
 Query Match 56.2%; Score 1824; DB 6; Length 1037;
 Best Local Similarity 55.2%; Pred. No. 2.5e-150;
 Matches 349; Conservative 97; Mismatches 134; Indels 52; Gaps 11;
 6 RFPSEW--IILCYWLLGFAHTGEAQAQAKVLLDSKAQOTLEWISSPPSGWEBSIGLDE 63
 DB 37 RAPLMWTLCLC-----AALRTLLASPSNEVNLDSRTVMDGLMIAPPKNGWEBSIGVDE 91

QY 64 NTPTIRTYOVCQWMEPNONNMILRTNWSKNAORIFVELKFTLRDQNSLPGLGTCKETP 123
DB 92 NVAPRHTYQVCKWMEQONNMILTSWISNEGASRIFFELKFTLRDQNSLPGLGTCKETP 151
QY 124 NLYYETDVTGKRNIRENLVYKIDITIAADESFTQGDIGERKMKLNTVEIRIPLSKKGFY 183
DB 152 NMVYFESDDQNGRNIRENOYIKIDITIAADESFTELDGDVYMKLNTVEIRIPLSKKGFY 211
QY 184 LAFQDVGACIALVSVKYYKKCWITVENLAVFPDITVGSFESSLVVERGTC/SSAEEBAE 243
DB 212 LAFQDVGACIALVSVKYYKKCWITVENLAVFPDITVGSFESSLVVERGTC/SSAEEBAE 269
QY 244 NSPRMHCASAGEMLVPIGKICCKAGYQOQKGTCEPCGRPRFYKSSODLQCSRCPTHSFSD 303
DB 270 EPRKMHCSAGEMLVPIGKICCKAGYEEKNGTCQVCPGPFKXSPHIQSGCKCPHSYTH 329
QY 304 REGSSRCECEDGYRRASDPYVACTRPPSAPONLFINIQTVLSLEWSPADNGRNDV 363
DB 330 EEAATSCVCEKDYFRRESDPPTWACTRPPSAPRNALSNVNETSVFLEWIPPADTGRKDV 389
QY 364 TYRILCKRCWEGECVPCGSNIGVMPQOTGLENDYVTVMDLAAHANYFEVEAVNGVSD 423
DB 390 SYTIACKCKSHAGVCECGGHVRYLPKQSGLKNTSVMMVDLAAHNYTFEIEAVNGVSD 449
QY 424 LSRQRLFAAVSITTTQGAAPSOVSGWKEKRVLQSVOLSQOEBEHPNGVITEXEIKYK 483
DB 450 LSPGARQYVSVNTTQGAAPSPVTNVKKGKIANKSISLSQOEBDRPGIILFYEIKYK 509
QY 484 DQRERTYSLTKYSTASINNLKPGTVYVFOIRAVTAAGYGNTPRLDVAITLEBASGMF 543
DB 510 DQ-ETSYTIKSKETITTAAGLKPASVYVFOIRARTAAGYVFSRRPE-----F 557
QY 544 EAT---AVSSEONPVIIIAVAVAGTIIIVMVFEGFII-----GRR----- 581
DB 558 ETPPVFAASSDQOIPYIAVSIVTG-VILAVVIGVILSSGCECGGKRAKSLCAVAHPS 616
QY 582 ---HCGYSKADQEGDEE-LYFHSLVTVNEHLSV 609
DB 617 LVRGYSKAKQDPEEKMEFH-----NGHKL 644

RESULT 10
ABG61868
ID ABG61868 standard; protein; 1037 AA.
XX ABG61868;
AC
XX
DT 15-AUG-2002 (first entry)
XX
DE Prostate cancer-associated protein #69.
XX
KM Prostate cancer; prostate tumour tissue; human; mammal; cyrstatic.
XX
OS Mammalia.
XX
PN WO200230268-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US032045.
XX
PR 13-OCT-2000; 2000US-00687576.
PR 08-DEC-2000; 2000US-00733288.
PR 08-DEC-2000; 2000US-00733742.
PR 24-JAN-2001; 2001US-0263957F.
PR 16-MAR-2001; 2001US-0276791P.
PR 16-MAR-2001; 2001US-0276888P.
PR 06-APR-2001; 2001US-0281922P.
PR 24-APR-2001; 2001US-0286214P.
PR 30-APR-2001; 2001US-00847046.
PR 04-MAY-2001; 2001US-0288589P.
XX

PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
PI WPI; 2002-471335/50.
XX
DR N-PSDB; ABK92183.
XX
PT Detecting a prostate cancer-associated transcript in a cell in a patient,
PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,
PT by determining if prostate cancer-associated genes are expressed in a
PT prostate tissue.
XX
PS Claim 27; Page 354; 436p; English.
XX
XX The present invention relates to methods of detecting a prostate cancer-
CC associated transcript in a cell from a patient. The method comprises
CC contacting a biological sample from the patient with prostate cancer-
CC associated polynucleotides (designated PC genes) that selectively
CC hybridize to a sequence that is at least 80% identical to them. The
CC prostate cancer-associated polynucleotide sequences are differentially
CC expressed in prostate tumour tissue or in prostate cancer and are derived
CC from the tissues of various organisms such as humans or other mammals
CC (e.g. mice, sheep and dogs). The methods of the invention are useful for
CC diagnosing and treating prostate cancer in mammals. The prostate cancer-
CC associated genes are useful for diagnosing or treating prostate cancer,
CC as well as for identifying modulators of prostate cancer or agents that
CC inhibit prostate cancer. The nucleic acid sequences are particularly
CC useful in gene therapy, as a vaccine or in antisense applications.
CC ABG61800-ABG61944 represent prostate cancer-associated proteins
XX
SQ Sequence 1037 AA;
Query Match 56.1%; Score 1819; DB 5; Length 1037;
Best Local Similarity 55.1%; Pred. No. 6, 7e-150;
Matches 348; Conservative 98; Mismatches 134; Indels 52; Gaps 11;
QY 6 RPSW--IILCYMLGFAHTGEAQAKEYLLDSQAQOTELEWISSPSSGMEISGLDE 63
DB 37 RAFLWTLCLLC-----AAKTLTLLASPSNEVNLDSRTVWGDLGWIAPKNGWBEIEVD 91
QY 64 NTPTIRTYOVCQWMEPNONNMILRTNWSKNAORIFVELKFTLRDQNSLPGLGTCKETP 123
DB 92 NVAPRHTYQVCKWMEQONNMILTSWISNEGASRIFFELKFTLRDQNSLPGLGTCKETP 151
QY 124 NLYYETDVTGKRNIRENLVYKIDITIAADESFTQGDIGERKMKLNTVEIRIPLSKKGFY 183
DB 152 NMVYFESDDQNGRNIRENOYIKIDITIAADESFTELDGDVYMKLNTVEIRIPLSKKGFY 211
QY 184 LAFQDVGACIALVSVKYYKKCWITVENLAVFPDITVGSFESSLVVERGTCVSSAEEBAE 243
DB 212 LAFQDVGACIALVSVKYYKKCWITVENLAVFPDITVGSFESSLVVERGTCVSSAEEBAE 269
QY 244 NSPRMHCASAGEMLVPIGKICCKAGYQOQKGTCEPCGRPRFYKSSODLQCSRCPTHSFSD 303
DB 270 EPRKMHCSAGEMLVPIGKICCKAGYEEKNGTCQVCPGPFKXSPHIQSGCKCPHSYTH 329
QY 304 REGSSRCECEDGYRRASDPYVACTRPPSAPONLFINIQTVLSLEWSPADNGRNDV 363
DB 330 EEAATSCVCEKDYFRRESDPPTWACTRPPSAPRNALSNVNETSVFLEWIPPADTGRKDV 389
QY 364 TYRILCKRCWEGECVPCGSNIGVMPQOTGLENDYVTVMDLAAHANYFEVEAVNGVSD 423
DB 390 SYTIACKCKSHAGVCECGGHVRYLPKQSGLKNTSVMMVDLAAHNYTFEIEAVNGVSD 449
QY 424 LSRQRLFAAVSITTTQGAAPSOVSGWKEKRVLQSVOLSQOEBEHPNGVITEXEIKYK 483
DB 450 LSPGARQYVSVNTTQGAAPSPVTNVKKGKIANKSISLSQOEBDRPGIILFYEIKYK 509
QY 484 DQRERTYSLTKYSTASINNLKPGTVYVFOIRAVTAAGYGNTPRLDVAITLEBASGMF 543
DB 510 DQ-ETSYTIKSKETITTAAGLKPASVYVFOIRARTAAGYVFSRRPE-----F 557
QY 544 EAT---AVSSEONPVIIIAVAVAGTIIIVMVFEGFII-----GRR----- 581

Db 558 ETPVFAASSDQSOIPVIAVSVTVG-VILLAVIGVLSSGCCGCCGRASSLCAVAHPI 616
Qy 582 ---HCGYSKADQEDDEE-LYFHSILVTNEHLSV 609
Db 617 LHMCGYSKAKODPEEKMHF---NGHITKL 644

RESULT 11
ADEJ31683
ID ADEJ31683 standard; procein; 1037 AA.
AC ADEJ31683;
XX 29-JAN-2004 (first entry)
XX Human 1419 protein #SEQ ID 40.
XX
XX Antiarteriosclerotic; cardiant; vasotrophic; antiinflammatory;
XX thrombolytic; antiarrhythmic; antianginal; hypotensive; gene therapy;
XX cardiovascular; disorder; ischaemia; aortic bending;
XX vascular heart disease; endocarditis; atrial fibrillation; heart failure;
XX angina; cardiomyopathy; cardiac death.
XX
XX Homo sapiens.
XX
XX WO2003065984-A2.
XX
XX 14-AUG-2003.
XX
XX 29-JAN-2003; 2003WO-US002571.
XX
XX 01-FEB-2002; 2002US-0353224P.
XX 15-MAR-2002; 2002US-0354529P.
XX 19-APR-2002; 2002US-0373861P.
XX 29-APR-2002; 2002US-0376287P.
XX 12-JUN-2002; 2002US-0388080P.
XX 24-JUN-2002; 2002US-0390971P.
XX 03-JUL-2002; 2002US-0394130P.
XX 10-JUL-2002; 2002US-0394797P.
XX 21-AUG-2002; 2002US-0404904P.
XX 23-AUG-2002; 2002US-0405450P.
XX 04-SEP-2002; 2002US-0408070P.
XX 06-NOV-2002; 2002US-0424300P.
XX 05-DEC-2002; 2002US-0431042P.
XX 05-DEC-2002; 2002US-0431079P.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Logan TJ, Chun M, Galvin KM, Healy A, Acton SL, Donaghu M,
XX Scagliano N, Perodin J, Rodrigue-Way A,
XX WPI, 2003-731468/69.
XX N-PSDB; ADEJ31682.
XX
XX Identifying a compound capable of treating a cardiovascular disorder
XX (e.g. atherosclerosis) comprises assaying the ability of the compound to
XX modulate the expression or activity of e.g. 1682, 6169 or 6193
XX polypeptide or nucleic acid.
XX
XX Disclosure; SEQ ID NO 40; 328bp; English.
XX
XX The invention relates to a method for identifying a compound capable of
XX treating a cardiovascular disorder. The present invention identifies the
XX differential expression of 1682, 6169, 6193, 7771, 14395, 29002, 33216,
XX 43126, 69292, 21656, 32427, 2402, 7747, 1720, 9151, 60491, 1371, 7077,
XX 33077, 1419, 18036, 16105, 38650, 14245, 58848, 1870, 25856, 33394, 3484,
XX 345, 9252, 9135, 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912,
XX 2868, 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914, 51130,
XX 19489, 21833, 22517, 59590, 15992, 2094, 2252, 3474, 9792, 15400, 1452 or
XX 6585 genes in cardiovascular disease states. The methods are useful in
XX diagnosing, preventing and treating cardiovascular disorders, such as
XX atherosclerosis, cardiac hypertrophy, ischaemia, reperfusion injury,

CC stenosis, arterial inflammation, vascular wall remodeling, coronary
CC microembolism, tachycardia, bradycardia, pressure overload, aortic
CC bending, coronary artery ligation, vascular heart disease, valvular
CC disease, including but not limited to, valvular degeneration caused by
CC calcification, rheumatic heart disease, endocarditis, or complications of
CC artificial valves; atrial fibrillation, long-QT syndrome, congestive
CC heart failure, sinus node dysfunction, angina, heart failure,
CC hypertension, atrial fibrillation, atrial flutter, pericardial disease,
CC including but not limited to, pericardial effusion and pericarditis;
CC cardiomyopathies, e.g. dilated cardiomyopathy or idiopathic
CC cardiomyopathy, myocardial infarction, coronary artery disease, coronary
CC artery spasm, ischaemic disease, arrhythmia, sudden cardiac death and
CC cardiovascular developmental disorders. The methods may also be used for
CC identifying compounds that modulate cardiovascular disorders. Sequences
CC given in ADEJ31644-ADEJ31769 represent the genes and proteins that may be
CC regulated by a compound of the invention.
XX
XX Sequence 1037 AA;
XX
XX
XX Query Match 56.1%; Score 1819; DB 7; Length 1037;
XX Best Local Similarity 55.1%; Pred. No. 6.7e-150;
XX Matches 348; Conservative 98; Mismatches 134; Indels 52; Gaps 11;
Qy 6 RPSW-ILICYIWLGFHTGEAQAKEVLLDSKAQOTELWISSPSSGWEISGIDE 63
Db 37 RAPLMTCLLLC-----AALRTILASPSENVLLDSRTVMGDLGVIAPKXGMEIIGEVDE 91
Qy 64 NYTPIRTYQVQVWPEPNQNMWLRFTNWSKGAQNIPEBLKTTLDNCNSLPVLTCKETP 123
Db 92 NYAPIHTYQVCKWEQNMNMLTWSINBQASRIPELKTPLDNCNSLPGLTGCKETP 151
Qy 124 NLYYETDYPDTRGIRNELYKIDITIADESFTQGDGERKMKNTREAREIGPLSKGFY 183
Db 152 NMYFESDQNGRIKENQIKITIDIADESFTLSDGRMKNTREYRDVGPLSKGFY 211
Qy 184 LAFQDVACIALVSVKYYKKCWITVENLAVFPDVTGSEBSLVEYRGTCVSSAEEBAE 243
Db 212 LAFQDVACIALVSVRYKKCPVNHVLAFFPTITIGADSQLLEVSGCVN--HSVTD 269
Qy 244 NSPRMCSAGEWLVPIGKCI CKAGYQOKGDTCPGCRFPFKSSQDLQCRCTHPSFD 303
Db 270 EPPMHCSAGEWLVPIGKCI CKAGYQOKGDTCPGCRFPFKASPHIQCCKCPHSYTH 329
Qy 304 REGSSRCECEGYRASPDPYVACTRPAPAKMLININQTTVSLSPSPADNGRNDV 363
Db 330 EEAISTCVCEDYFRRESDEPTMACTRPAPAKMLININQTTVSLSPSPADNGRNDV 389
Qy 364 TYRILCRSGWQECVPCGSNIGYMPQGTLEBNYTVMDLLAHANYTFEVEAVNGVSD 423
Db 390 SYTLACKKSHAGVCECGHRYVLPKRGSLKNTSVMDLANTHTYTFEIVANGVSD 449
Qy 424 LRSQRLFAVSTTGAAPDSQVSGMKERYLORSVOLSWOEPHPNGVITYEIKYK 483
Db 450 LSPGARQVSVNTVTPNAAAPSVTVKKGKIAKNSISLSWOEPHPNGIILEYEIKHPEK 509
Qy 484 DQERTSTLTXTSTASINNLRKGYVFOIRVTAAGVYSPRIQVATLEASGMF 543
Db 510 DQ-ETSTYTIKSKETITTAGLKPASVYFOIRKRIAGVGFVRRPE-----F 557
Qy 544 EAT---AVSEONFVITIAVAVAGTITLVFMVGFIT-----GRR----- 581
Db 558 ETPVFAASSDQSOIPVIAVSVTVG-VILLAVIGVLSSGCCGCCGRASSLCAVAHPI 616
Qy 582 ---HCGYSKADQEDDEE-LYFHSILVTNEHLSV 609
Db 617 LHMCGYSKAKODPEEKMHF---NGHITKL 644

RESULT 12
ABP52827 standard; protein; 975 AA.
XX
XX ID ABP52827
XX AC ABP52827;


```

FT      /note= "HLA class I binding motif"
FT      Binding-site
FT      727..735
FT      /note= "HLA class I binding motif"
FT      Binding-site
FT      788..796
FT      /note= "HLA class I binding motif"
FT      Binding-site
FT      895..903
FT      /note= "HLA class I binding motif"
FT      Binding-site
FT      929..937
FT      /note= "HLA class I binding motif"
XX
XX      W0200050589-A1.
XX
XX      31-AUG-2000.
XX
XX      18-FEB-2000; 2000MO-US004326.
XX
XX      22-FEB-1999; 99US-0121170P.
XX      PR      08-OCT-1999; 99US-0158566P.
XX
XX      (LUDW-) LUDWIG INST CANCER RES.
XX
XX      Chiari R, Coulie P, Boon-Falleur T;
XX
XX      WPI; 2000-572089/53.
XX      N-PSDB; AAA64458.
XX
XX      Novel tyrosine kinase receptor, EphA3 human leukocyte antigen (HLA) class
XX      PT      II binding peptide and nucleic acid encoding the receptor, useful for
XX      PT      diagnosing and treating conditions characterized by expression of EphA3
XX      PT      gene.
XX
XX      Claim 1; Page 81-83; 107pp; English.
XX
XX      The present sequence represents a EphA3 HLA (human leukocyte antigen)
XX      CC      class II-binding peptide. EphA3 antigens, when presented by an antigen
XX      CC      presenting cell having a HLA class II molecule, effectively induce
XX      CC      activation and proliferation of CD4+ T lymphocytes. EphA3 is a tumour
XX      CC      associated gene. EphA3 HLA binding peptides are used for selectively
XX      CC      enriching a population of T lymphocytes. The peptides are also used for
XX      CC      diagnosing a disorder characterized by EphA3 or EphA3 HLA binding peptide
XX      CC      expression. The peptides are also used to treat a disorder characterized
XX      CC      by EphA3 expression. The EphA3 binding peptides are useful in producing
XX      CC      vaccines and antibody
XX
XX      Sequence 983 AA:
XX
XX      Query Match      55.5%; Score 1799; DB 3; Length 983;
XX      Best Local Similarity 57.0%; Pred. No. 3.5e-148;
XX      Matches 332; Conservative 103; Mismatches 131; Indels 16; Gaps 6;
XX
Oy      28 QAAKEVLLDSKQQTLEWISSPSPGMEISGLDENVTPIRYOVQVMEPNOMNMLRT 87
Db      25 QPSNEVALLDSKQQTLEWISSPSPGMEISGLDENVTPIRYOVQVMEPNOMNMLRT 84
Oy      88 NWISKGAORIFVELKFTLRDCLNSLPGLGCTKETFPILYYETDYDGRNIRELKYIKD 147
Db      85 NWVPRNAQKTYELKFTLRDCLNSLPGLGCTKETFPILYYESDDDGAKEREHQFKID 144
Oy      148 TIAADESFTQDGERKMKLNTVEIREIGPLSKKGFYAFQDVAGACIALVSVKYYKKCWT 207
Db      145 TIAADESFTQMDLDRILKLNTEIREVGPVKKGFYAFQDVAGACIALVSVRYFKKCPF 204
Oy      208 IVENLAFPTVTVGSEFSSLVENVGTQVSSAEAEASPMHGCABEEMLVPIGKICKA 267
Db      205 TVKNLAFPTVTVGSEFSSLVENVGTQVSSAEAEASPMHGCABEEMLVPIGKICCA 261
Oy      268 GYOQKQDTCPCGRRFYKSSSODLQCRPTSPFSDESSRCCEDEGYAPSPDPYVA 327
Db      262 GYBERGFMCGACRGCFYKALDGNMKKAKCPHSSFTQDGSNMGCENNYPPADDPSPMA 321
Oy      328 CTRPPSPAPNLIPIINOTTVSLSEWSPPADNGRNDVYTRILCKRCSNQECEVPGCSNIG 387
Db      322 CTRPPSPSPRVNISINETSIVLIDWSWPLDTGGRKDVTFNII CKKCGNNIKCEPCSPNVR 381

```

```

Oy      388 YMPQQTGLFDNYTVMDLHLAHANYFEVAVNGVSDLSRQRLPFAVSIITGQAAPSOVS 447
Db      382 FLPRQFGLNTVTVYDVLHNTVTEPIDAVNGVSELSPPROPAAVSIITNOAABPVL 441
Oy      448 GWMKERVLOSVOVLSWQEPHPNGVITEYEIKYKQDQRETYSTLTKTSASINNLKP 507
Db      442 TIKDRTSRNSISLSWQEPHPNGIILDEVKTYKEQGETSYTILARGTNVITSLKP 501
Oy      508 GTTVVFOIRAVTAAGYNTSPRLDVATLEASGKMPATVSSQONVITIIAVAVAGTI 567
Db      502 DTIVVFOIRARTAGVGTNRKKEFTSP-----DSFSISGSSQVMAISAAYAI 554
Oy      568 ILEVMPFGFIIGRRHCGSKADQGEDELYEHSLVTEHLSV 609
Db      555 LITVVIY-VLIG-RFCGYKSKRGADKRLHF----GNGHLKL 590
XX
XX      RESULT 14
XX      ID      AAB08666 standard; protein; 983 AA.
XX
XX      AC      AAB08666;
XX
XX      DT      02-JAN-2001 (first entry)
XX
XX      DE      A human EphA3 HLA class II-binding peptide.
XX
XX      KW      EphA3; HLA class II-binding peptide; human leukocyte antigen; antigen;
XX      KM      CD4+ T lymphocyte; tumour associated gene; vaccine.
XX      OS      Homo sapiens.
XX
XX      PN      W0200050589-A1.
XX
XX      PD      31-AUG-2000.
XX
XX      PF      18-FEB-2000; 2000MO-US004326.
XX
XX      PR      22-FEB-1999; 99US-0121170P.
XX      PR      08-OCT-1999; 99US-0158566P.
XX
XX      PA      (LUDW-) LUDWIG INST CANCER RES.
XX
XX      PI      Chiari R, Coulie P, Boon-Falleur T;
XX
XX      WPI; 2000-572089/53.
XX      N-PSDB; AAA64459.
XX
XX      Novel tyrosine kinase receptor, EphA3 human leukocyte antigen (HLA) class
XX      PT      II binding peptide and nucleic acid encoding the receptor, useful for
XX      PT      diagnosing and treating conditions characterized by expression of EphA3
XX      PT      gene.
XX
XX      Claim 1; Page 88-90; 107pp; English.
XX
XX      The present sequence represents a EphA3 HLA (human leukocyte antigen)
XX      CC      class II-binding peptide. EphA3 antigens, when presented by an antigen
XX      CC      presenting cell having a HLA class II molecule, effectively induce
XX      CC      activation and proliferation of CD4+ T lymphocytes. EphA3 is a tumour
XX      CC      associated gene. EphA3 HLA binding peptides are used for selectively
XX      CC      enriching a population of T lymphocytes. The peptides are also used for
XX      CC      diagnosing a disorder characterized by EphA3 or EphA3 HLA binding peptide
XX      CC      expression. The peptides are also used to treat a disorder characterized
XX      CC      by EphA3 expression. The EphA3 binding peptides are useful in producing
XX      CC      vaccines and antibody
XX
XX      Sequence 983 AA:
XX
XX      Query Match      55.5%; Score 1799; DB 3; Length 983;
XX      Best Local Similarity 57.0%; Pred. No. 3.5e-148;
XX      Matches 332; Conservative 103; Mismatches 131; Indels 16; Gaps 6;

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QY 28 QAAKEVLLDLSKAOQTELEWISSPPSGMEISGLDENYTPRTYQVCVMEPNQNNWLT 87
DB 25 QPSENEVLLDLSKTIQDELWISYPSHGWIEISGVDEHYTPRTYQVCVMEPNQNNWLT 84
QY 88 NMWISKNAORIFVELKFTLRDCNSLPGLVGTCKETFNLYYYETDYDGRINRENLVYKID 147
DB 85 NMVPRNSAQKIYVELKFTLRDCNSIPVLGTCKETFNLYYMESDDHGVKFRHQFTKID 144
QY 148 TIAADESFTQGDIGERRMKLNTVEIREIGPLSKKGFYLAFOVAGACIALVSVKYYKKCMT 207
DB 145 TIAADESFTQMDIGDRILKLNTEIREVGPVNNKGFYLAFOVAGACIALVSVRYFKKCP 204
QY 208 IYENLAVFPDPTVYGSSESLVEVRGTCVSSAEBAENSPPMCSAGSEMLVPIGKICCKA 267
DB 205 IYVNLAMFPDPTV-MDSQSLVEVRGSCVNNKSKE--EDPPMYCSTEGEWLVPIGKICSCNA 261
QY 268 GYOQKDGTCPCGRFRFYKSSODLQCRCPHSSFDRESSRCEDDGYVYAPSDPPYVA 327
DB 262 GYERGFMCQACRPGFYKALDGNMKCAKCPHSSSTQDGSMMNCRCENNYFLADKDPSPMA 321
QY 328 CTRPSPAPQNLIFNINQTTVSLSEWSPPADNGRNDVTYRILCKRCSWEQIGCVPCGSNTG 387
DB 322 CTRPSPSPRVNIVSNINETSVIDLMSWPLDTGGRKDVTFNIIICKCGMNIKQCEPCSPNV 381
QY 388 YMPQQTGLENDYVTWDLAHANYTFEVEAVNGVSDLSRQRLFAVSTITGQAAPSOVS 447
DB 382 FLPRQGLTNTYTVTDLHAHTYTFEIDA VNGVSELSPRQFAVSTITGQAAPSPVL 441
QY 448 GNMKERVLRQSVOLSMQEPHPNGVITEYEIKYKEDQERTYSTLKTSYASINNLKP 507
DB 442 TIKKDRISRSISLSMOEPHPNGIILDYEVKYEKQEOETSTYLIRAGTNTVTSLSKP 501
QY 508 GTVYVFOIRAVTAAGYGNVSPRLDVATLEASGKMEFATVSSBQNVIIIAVAVAGTI 567
DB 502 DTIYVFOIRARTAGYGNSTSRKEFEFTSP-----DSFISGESSQVVMIAISAVALI 554
QY 568 ILVFMVFGFIIGRRHCGYSKADQEGDELYFHSVTNREHLSV 609
DB 555 LITVIVY-VLIG-RFCGYKSKHGADKRLHF---GNGHLK 590

RESULT 15
ABR57491
ID ABR57491 standard; protein; 983 AA.
XX
AC ABR57491;
XX
DT 16-SEP-2003 (first entry)
XX
DE Human EphA3 protein SpQ ID NO:11.
XX
KW Human; bone and joint diseases; antiarthritic; antirheumatic; osteopathic;
KM antiinflammatory; arthritis deformans; chronic rheumatoid arthritis;
KW synovial inflammation; arthritis; tennis elbow; EphA3; Eph receptor A3.
XX
OS Homo sapiens.
XX
PN WO2003022300-A1.
XX
PD 20-MAR-2003.
XX
PF 09-SEP-2002; 2002WO-JP009140.
XX
PR 10-SEP-2001; 2001JP-00273914.
PR 17-SEP-2001; 2001JP-00281472.
PR 28-SEP-2001; 2001JP-00300289.
PR 28-SEP-2001; 2001JP-00300347.
PR 28-SEP-2001; 2001JP-00300417.
PR 28-SEP-2001; 2001JP-00303390.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
PI Hikichi Y, Inazuka M, Yoshimura K;
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XX WIPI; 2003-313193/30.
DR N-PSDB; ACF03675.
XX
PT Substances regulating the activity of proteins having increased
PT expression in bone and joint disease for treatment and prevention of
PT these diseases.
XX
PS Claim 1; Page 132-136; 154p; Japanese.
XX
CC The present invention describes agents (A) for treating and preventing
CC bone and joint diseases. (A) regulate the activity or expression of human
CC proteins (I) which show increased expression in diseased bone and joint
CC tissue e.g. D102 (type 2 Iodothyronine deiodinase); ANKH (pyrophosphate
CC transporter); SHOX2 (short stature homeobox 2); TSK4 (potassium ion
CC channel protein); EphA3 (Eph receptor A3); and/or MMP16 (matrix
CC metalloproteinase 16). (A) have antiarthritic, antirheumatic, osteopathic
CC and antiinflammatory activities. (A) can be used for the prevention,
CC treatment and diagnosis of diseases involving the abnormal formation or
CC development of bone and cartilage (such as arthritis deformans), chronic
CC rheumatoid arthritis, synovial inflammation, or localised arthritis (such
CC as tennis elbow). The present sequence represents human EphA3, from the
CC present invention
XX
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SQ Sequence 983 AA;

Query Match 55.5%; Score 1799; DB 6; Length 983;

Best Local Similarity 57.0%; Pred. No. 3,5e-148;

Matches 332; Conservative 103; Mismatches 131; Indels 16; Gaps 6;

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QY 28 QAAKEVLLDLSKAOQTELEWISSPPSGMEISGLDENYTPRTYQVCVMEPNQNNWLT 87
DB 25 QPSENEVLLDLSKTIQDELWISYPSHGWIEISGVDEHYTPRTYQVCVMEPNQNNWLT 84
QY 88 NMWISKNAORIFVELKFTLRDCNSLPGLVGTCKETFNLYYYETDYDGRINRENLVYKID 147
DB 85 NMVPRNSAQKIYVELKFTLRDCNSIPVLGTCKETFNLYYMESDDHGVKFRHQFTKID 144
QY 148 TIAADESFTQGDIGERRMKLNTVEIREIGPLSKKGFYLAFOVAGACIALVSVKYYKKCMT 207
DB 145 TIAADESFTQMDIGDRILKLNTEIREVGPVNNKGFYLAFOVAGACIALVSVRYFKKCP 204
QY 208 IYENLAVFPDPTVYGSSESLVEVRGTCVSSAEBAENSPPMCSAGSEMLVPIGKICCKA 267
DB 205 IYVNLAMFPDPTV-MDSQSLVEVRGSCVNNKSKE--EDPPMYCSTEGEWLVPIGKICSCNA 261
QY 268 GYOQKDGTCPCGRFRFYKSSODLQCRCPHSSFDRESSRCEDDGYVYAPSDPPYVA 327
DB 262 GYERGFMCQACRPGFYKALDGNMKCAKCPHSSSTQDGSMMNCRCENNYFLADKDPSPMA 321
QY 328 CTRPSPAPQNLIFNINQTTVSLSEWSPPADNGRNDVTYRILCKRCSWEQIGCVPCGSNTG 387
DB 322 CTRPSPSPRVNIVSNINETSVIDLMSWPLDTGGRKDVTFNIIICKCGMNIKQCEPCSPNV 381
QY 388 YMPQQTGLENDYVTWDLAHANYTFEVEAVNGVSDLSRQRLFAVSTITGQAAPSOVS 447
DB 382 FLPRQGLTNTYTVTDLHAHTYTFEIDA VNGVSELSPRQFAVSTITGQAAPSPVL 441
QY 448 GNMKERVLRQSVOLSMQEPHPNGVITEYEIKYKEDQERTYSTLKTSYASINNLKP 507
DB 442 TIKKDRISRSISLSMOEPHPNGIILDYEVKYEKQEOETSTYLIRAGTNTVTSLSKP 501
QY 508 GTVYVFOIRAVTAAGYGNVSPRLDVATLEASGKMEFATVSSBQNVIIIAVAVAGTI 567
DB 502 DTIYVFOIRARTAGYGNSTSRKEFEFTSP-----DSFISGESSQVVMIAISAVALI 554
QY 568 ILVFMVFGFIIGRRHCGYSKADQEGDELYFHSVTNREHLSV 609
DB 555 LITVIVY-VLIG-RFCGYKSKHGADKRLHF---GNGHLK 590
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